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GenCore version 4.5
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OM protein - protein search, using sw model

April 13, 2001, 15:34:33 ; Search time 32.39 Seconds (without alignments) 256.730 Million cell updates/sec Run on:

US-08-700-737-9 658 1 QVQLQQPGAELVKPGTSVKL.....DGWDYAIDYWGQGTSVTVSS 121 Perfect score:

Sequence:

Scoring table:

198801 seqs, 68722935 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

198801 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description		chain V	neavy chain	lbody rap Jel	neavy chain pr	neavy chain V	neavy chain	r reader/19 he	neavy chain V	neavy chain pr	neavy chain V	neavy chain	neavy chain	heavy	gamma cha	gamma -	heavy cha	heavy chain pi	heavy chain	heavy	gamma chain	neavy	heavy	heavy chain v	neavy cha	heavy cha	heavy chain	i-glyc	cha	neavy chain
	ID	B22769	S41394	\$53751	E32513	520646	MHMS18	PC4402	525175	JI.0076	\$20643	B27563	03050	A27472	238050	540295	20000	110000	530024	276307	71020	D1,0208	26633	10000	C22563	110071	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	240000	27/049	HVMST7	
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	Length	120	120	116	138	123	139	287	120	141	122	117	118	131	246	446	13.5	130	122	21.	126	136	131	113	115	136	110	110	120	138	
æ	Query	-	ö	79.0	8	œ	æ	m.	œ.	ζ.	ζ.	'n		٠.,	٠.,	٠:		•	: :		٠.	• •			٠	- 2	•	•	•	72.6	
	Score	3	527.5	-	516		514.5		514	507.5	507	499.5	õ	495	495	495	492.5	6	491.5	489	488.5	4	w	484.5	83	83	4	481	479.5		
	Result No.	П	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	29	

heavy	heavy	chain	heavy chain	heavy chain	heavy chain	neavy chain	neavy chain	hoavy chain	neavy chain	neavy chain	neavy chain	heavy	
2 S25048 2 S25044	2 PH1160	2 S25052	2 A26405	2 F2938U	2 636302	2 525047	2 S25024	2 509956	2 PL.0089	2 525032	2 225025	2 \$26309	
111	98	111	121	110	123	111	111	120	119	111	11	116	
72.6	72.5	72.3	72.0	71.9	71.9	71.8	71.8	71.8	71.7	71.7	71.7	71.5	
477.5	477	475.5	474	473	473	472.5	472.5	472.5	472	471.5	471.5	470.5	
30	32	3.0	3 2	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT B22769

Ig heavy chain V region (B1-8.VI/V2) - mouse (tentative sequence) C;Species: Mus musculus (house mouse) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996 C;Accession: B22769 C;Accession: Carlo Callo C;Accession: Callo Callo C;Accession: Callo Callo C;Accession: Callo Callo C;Accession: Callo
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DB 2; Length 120; Score 533.5; DB 2 Pred. No. 6.5e-40; 5; Mismatches 13 F;15-98/Domain: immunoglobulin homology <IMM> Query Match 81.1%; SC Best Local Similarity 84.3%; Pr Matches 102; Conservative 5;

ij 61 NOKFKGRATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWGQGTSVTVS 120 Gaps 1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60 ä Indels 13; g ò QQ ô

S 121 s 120 121 120 ò QQ

RESULT 2
\$41394

Ideavy chain V region - mouse

Cj Species: Mus musculus (house mouse)
Cj Species: S41394
R; Margaritte, C.; Gilbert, D.; Brard, R.; Tron, F.
Submitted to the EMBL Data Library, January 1994
A; Description: Structural characterization of an (NZB X NZW)F1 mouse-derived Igm anti
A; Reference number: \$41393
A; Accession: \$41394
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-120 < WAR>
A; Residues: 1-120 < WAR>
A; Cross-references: EMBL: Z29586; NID: 9452354; PIDN: CAA82703.1; PID: 91334080

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Ig heavy chain precursor V region (B1-8) - mouse
N.Contains: Ig heavy chain precursor V region 186-2
Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A90809; B90809; A22769; A02034; A02036
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A;Reference number: A90809; MuID:81234548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Decession: 520646
F;Losman, M.; Pasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice 1
A;Reference number: $20639
A;Reference number: $20646
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A;Accession: B90809
                                                                                                                               Gaps
                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:X65001; NID:952612; PIDN:CAA46134.1; PID:952613 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                     1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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                                                                       Length 138;
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Pred. No. 2.7e-38;
9; Mismatches 11;
                                                                             516; DB 2;
No. 2.5e-38;
                                                                                                                                     6; Mismatches
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                   Score Pred.
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Local Similarity 79.2%;
les 99; Conservative
                                                                             78.4%;
nilarity 82.6%;
Conservative 6
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A; Residues: 1-139 <B18>
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A; Residues: 1-123 <LOS>
                                                                                                             Best_Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus () musculus () c;Species: Mus musculus () 
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A;Residues: 1-138 <KOF>
A;Resiredrences: GB:M20835, NID:g196945; PIDN:AAA38847.1; PID:g196946
A;Crossrrefrences: GB:M20835, NID:g196945; pidm:nnoglobulin homology
C;Superfeily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                       Length 120;
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A;Residues: 1-116 <POK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;Is-98/Domain: immunoglobulin homology <IMM>
                    immunoglobulin homology
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Pred. No. 1e-38;
3; Mismatches 10;
                                                                                                                                                                DB 2;
                                                                                                                                                                Score 527.5; DB 2
Pred. No. 2.2e-39;
                                                                                                                                                                                                                     4; Mismatches
                                C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                             region;
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83.6%;
                                                                                                                                                                   85.18;
                          immunoglobulin V
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Best Local Similarity 83.65
Matches 102; Conservative
                                                                                                                                                                         Query Match
Best Local Similarity 85.1
Matches 103; Conservative
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A; Molecule type:

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If heavy chain V region - mouse

C. Species: Mus musculus (house mouse)
C. Accession: S25175
R. Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
S. B. Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
A. Pescription: Structure and binding properties of monoclonal antibodies to core hist.
A. Accession: S25175
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-120 < MONA
A. Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment) C; Species: Mus musculus (house mouse) C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999 C; Accession: JL0076 R; Kaartinen, M.; Rocca-Serra, J.; Maekelae, O. R; Kaartinen, M.; Rocca-Serra, J.; Maekelae, O. A; Title: Combinatorial association of V genes: one VH gene codes for three non-cross-A; Reference number: JL0076; MuID:89096973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYAIDYWGQGTSVTV 119
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A:MOLECULE type: mRNA
A:Molecule type: mRNA
A:Residues: 1-141 < KAAA>
A:Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Superfamily: isgnal sequence #stratus predicted <SIG>
F:1-19/Domain: signal sequence #stratus predicted <AIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:135-141/Region: Complementarity-determining 2
F:136-141/Region: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 514; DB 2;
Pred. No. 3.3e-38;
8; Mismatches 12;
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80.2%; Pred. No. 1.4e-37
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Best Local Similarity 81.8%;
Matches 99; Conservative
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Best Local Similarity
Matches 97; Conserv
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                                                       hapd
A; Residues: 1-117-41862>
A; Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt A; Note: the 186-2 germiine gene was cloned from a library of C57BL/6 DNA R; Didrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K. A; Tibre: Immunoglobulin V region variants in hybridoma cells. II. Recombination between A; Reference number: A90971; MUID:84236026
                                                                                                                                                                                                                                                   A; Molecule type: protein A; Molecule type: protein A ^{\rm A} A ^{\rm A} Relatues: 20-139 <DIL>A; Most the V region of the B1-8 delta chain, derived as a spontaneous class switch variative mu chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein - C;Species: synthetic C;Date: 06.Nov-1998 #sequence_revision 06.Nov-1998 #text_change 06.Nov-1998 #Suzuki, C:; Ueda, H.; Suzuki, E.; Nagamune, T. A;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T. A;Title: Construction, bacterial expression, and characterization of hapten-specific sin A;Reference number: PC4402 A;Accession: PC4402
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                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Introns: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
F:1-19/Domain: signal sequence *status predicted <SIG>
F:20-139/Product: Ig Rapaa chain V region (B1-8) *status experimental <MAT>
F:14/Region: D segment
F:118-124/Region: J segment
F:125-139/Region: J segment
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Best Local Similarity 81.0%; Pred. No. 3.4e-38;
Matches 98; Conservative 5; Mismatches 17
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5; Mismatches
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ilarity 81.08;
Conservative
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A; Wolecule type: DNA
A; Residues: 1-287 <SUZ>
C; Keywords: fusion protein
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Matches 98;
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1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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Pred. No. 1.6e-36;
3; Mismatches 13;
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                                                                                                                                                                                                                                Ig heavy chain V region (35.8.2H) - mouse (fragment)
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Pred. No. 7.2e-37;
4; Mismatches 17
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F;118-125/Region: complementarity-determining 3
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82.6%;
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Best Local Similarity
Matches 95; Conserv
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A; Residues: 1-118 <MA
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Best Local S
Matches 97
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A; Residues: 1-117 < CAR>
A; Residues: 1-117 < CAR>
A; Residues: 1-117 < CAR>
A; Cossoreferences: GB: M14974; NID: 9195260; PIDN: AAA38226.1; PID: 9195261
A; Cross-references: GB: M14974; NID: 9195260; PIDN: AAA38226.1; PID: 9195261
A; Note: this sequence was determined from the differentiated gene
A; Note: this sequence was determined from the differentiated gene
A; Note: the authors translated the codon GGT for residue 54 as Ala and TAC for residue
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
F;12-95/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from autoimmune MRL mice react
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                                                                                                                                                                                                                                                               Ly neavy chain V region - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999 C; Accession: 82064 M.; Fasy, T. M.; Novick, K.E.; Monestier, M. Sasy, T. M.; Novick, K.E.; Monestier, M.; Fasy, T. M.; Novick, R.E.; Monestier, M. A; Fasy, T. M.; Novick, R.E.; Monestier, M. A; Reference number: 820639 A; Accession: 820643 A; Accession: 820643 A; Accession: S20643 A; Accession: Proliminary A; Molecule type: DNA A; Residinary A; Molecule type: DNA A; Residinary A; Resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ig heavy chain V region (T14) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999
C;Accession: B27563
R;Carmack, C.E.; Pincus, S.H.
J; Immunol. 137, 3983-3989, 1986
A;Title: Variable regions of antibodies to synthetic polypeptides. II. Analy A;Reference number: A92812; MUID:87059009
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                                  --- DYWGOGTTLTVS 134
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A; Cross-references: EMBL:X64998; NID:g52606; PIDN:CAA46131.1; PID:g52607
A; Cross-references: EMBL:X64998; NID:g52606; PIDN:CAA46131.1; PID:g52607
C; Superfamily: immunoglobulin vegion; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.3e-37;
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10; Mismatches 1.
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80.68;
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Matches 100; Conserv
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C; Species: Mus musculus (house mouse)
C; Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C; Accession: 338950
R;Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(A; Accession: 538950)
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Submitted to the EMBL Data Library, January 1993
Abescription: Primary Structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: $40295
A;Accession: $40295
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C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:360-427/Domain: immunoglobulin homology <IMM>
F:14Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:22-96,144-199,261-321,367-425/Disulfide bonds: interchain (to 119ht chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:237/Binding site: carbohydrate (Asn) (covalent) #status experimental
                         61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGT 115
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-446 (KLE)
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 137-201/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 76.9%
Matches 93; Conservative
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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 75.2%; Score 495; DB 2; Length 44 illarity 76.9%; Pred. No. 5.9e-36; Conservative 10; Mismatches 14; Indels
75.2%;
76.9%;
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GenCore version 4.5
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OM protein . protein search, using sw model

April 13, 2001, 15:35:47 ; Search time 21.32 Seconds (without alignments) 194.414 Million cell updates/sec Run on:

US-08-700-737-9 658 658 1 QVOLQQPGAELVKPGTSVKL.....DGWDYAIDYWGQGTSVTVSS 121 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	B ID	Ě	HV50	_					1 HV09_MOUSE							HV49								HV42			HV4		HVOI					HV3J_HUMAN
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78.2%; Score 514.5; DB 1; Length 139;
Best Local Similarity 81.0%; Pred. No. 1e-44;
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P06326 homo sapien P01742 homo sapien P01768 homo sapien P01801 mus musculu P01772 homo sapien P01799 mus musculu P01799 mus musculu P01760 homo sapien P01804 mus musculu P01804 mus musculu P01796 mus musculu P01796 mus musculu	ita; Euteleostomi; idae; Murinae; Mus. (ari T., Rajewsky K., the NPb family of 2a variable region."; ONED FROM A HYBRIDOMA	e no re s conten y //www.1s //www.1s conten CION B1- ERMINING ERMINING CRC64;
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Eupkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                              80 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYCARYDYYGSSY-FDYWGQGTTLIVS
QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                   20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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pred. No. 2.7e-41;
7; Mismatches 22;
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23-OCT-1986 (Rel. 02, Last Sequence update)
24-ULL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                   120 AA.
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D SEGMENT.
J SEGMENT.
BY SIMILAR
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illarity 75.2%;
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Best Local Similarity
Matches 91; Conserv
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DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- MISCELLANBOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MARING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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MEDLINE-81234548; Pubmed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                               to C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                  "Illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984). PIR; A02033; HVMST7.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION S43 PRECURSOR.
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138 AA;
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Best Local Similarity
Matches 91; Conserv
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SA 138
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P01755;
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NCBI_TaxID=10090;
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Best Local Simi
Matches 89;
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P01747;
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HV03_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCAR---GGYDGWDYAIDYWGQGTSV 117
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION 93G7 PRECURSOR.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                       FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                        HEAVY CHAIN V REGION S43
                                                                                                                                                                                                                                 FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                             FRAMEWORK 3.
D SEGMENT.
send an email to license@isb-sib.ch),
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                                     EMBL; J00539; AAA38172.1; -.
PIR; A02039; G2MS43.
InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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137
137 AA;
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HV02_MOUSE
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MEDLINE-83131846; PubMed-6186498;
MEDLINE-83131846; PubMed-6186498;
MEDLINE-83131846; PubMed-6186498;
Marshak-Rothstein A.;
The Genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
The Genetic basis of antibody Production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Fur. J. Immunol. 12:1023-1032(198).

-I- MISCELLANBOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME JETS, AC2028; MANGEY.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                            IG HEAVY CHAIN V REGION 93G7.
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1 19 1G HEAVY CHAIN V REGION 9
140 140 140 1514 MW; 25A4CBBE31DA5CE8 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 36-65.
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                                                                                                                                                                    Similarity 73.6
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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HV06_MOUSE
ID HV06_MC
AC P01750;
DT 21-JUL-
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Signal.

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[mmunoglobulin V
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HV05_MOUSE
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                                                                                                                                           "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-1- MISCELLANDOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  2 VQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYN 61
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                                                                                                    STRATN=CS7BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                          Score 464; DB 1;
Pred. No. 9.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01753; P11271; 21-JUL-1986 (Rel. 01, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 01-JUL-1999 (Rel. 38, Last sequence update) IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 QKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCA 97
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3; Mismatches
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117 IG HI
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MEDLINE-81234548; PubMed-6788376;
                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Local Similarity 90.6%;
hes 87; Conservative 3
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                             InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region;
                                        Mus musculus (Mouse)
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117 AA:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                      QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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MEDILNE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                              IG HEAVY CHAIN V REGION 186-1. FRAMEWORK 1.
                                                                     COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                             Length 117;
                                                                                                          COMPLEMENTARITY - DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING
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                                                                                                                                                                                       12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 452; DB 1;
Pred. No. 1.4e-38;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 98
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15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 3 PRECURSOR.
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pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00536; AAA38605.1; -. PIR; A02031; HVMS3.
                                                                                                                                                                                                                                                     68.7%;
85.7%;
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Best Local Similarity 85.77
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
region;
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81
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P01749:
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Best Local Similarity 69.4'
Matches 84; Conservative
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                                                       SEQUENCE FROM N.A.
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                                  NCBI_TaxID=10090;
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P01748;
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                                                                                                                                                                                                                                                                                                                                                      "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains."; Blochemistry 21:3415-3424(1982).

-I- MISCELLANEOUS: THE SEQUENCE THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
-I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NOKEKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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                                                                                                                                                                                                                                                                                                                       MEDLINE-83075344; Pubmed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
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                Score 451; DB 1; Length 117;
Pred. No. 1.8e-38;
4; Mismatches 8; Indels
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55 55 N-LINKED (GLCNAC. .).
117 117 AA: 12983 MW; 3CF8ACE4BE447E41 CRC64;
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InterPro: IPR003006; -
Fram: PF00047; 1g; 1.
Immunoglobulin V region; Glycoprotein.
2 2 85 N-LINKED (GLCNAC.
                                                                                                                 67.9%; Score 447; DB 1;
71.1%; Pred. No. 4.6e-38;
iive 12; Mismatches 19
                                                                                                    61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 98
                                                                                                                                                                                                     71-Jul-1986 (Rel. 01, Created)
21-Jul-1986 (Rel. 01, Last sequence update)
15-Jul-1999 (Rel. 38, Last annotation update)
IG HENVY CHAIN V REGION MOPC 104E.
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               ch 68.5%;
l Similarity 87.8%;
86; Conservative
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                     Local Similarity
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P01756;
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P01745;
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Matches 86
               Query Match
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                 MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSE!
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 447; DB 1; Length 121; 69.4%; Pred. No. 4.8e-38; 1.ve 12; Mismatches 25; Indels
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SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDOBF CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAYY CHAIN V REGION 23 PRECURSOR.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                               MEDLINE-84182519; PubMed-6201362;
MIDITOP R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
Dildrop R., Bovens J., Siekevitz M., Beyreuther R., Rajewsky R.;
"A V region determinant (idiotope) expressed at high frequency in B
"Imphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW; 94F7BEE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.1%; Score 441.5; DB 1;
70.5%; Pred. No. 1.6e-37;
iive 11; Mismatches 20;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 205.12.
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J SEGMENT.
BY SIMILARITY.
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Cell 40:271-281(1985).
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Matches 86; Conser
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P06328;
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HV49_MOUSE
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                                                                                                                                                                                                                                                                    Gaps
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Nature 283:35-40(1980).
-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
WHICH OCCUR IN THE D AND J SECMENTS.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Schilling J., Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran and DNA
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                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                          Query Match 67.6%; Score 445; DB 1; Length 11 Best Local Similarity 84.7%; Pred. No. 7.2e-38; Matches 83; Conservative 2; Mismatches 13; Indels
     FRAMEWORK 2. COMPLEMENTARITY-DETERMINING
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                                                                                                                                    12772 MW; C530F829C906F69B CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Pfam; PF00047; ig; 1.
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HV51_MOUSE
ID HV51_MOUSE
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P01757;
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IG HEAVY CHAIN V REGION VH558 B4.
FRAMEWORK 1.
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Gaps ; 0 Query Match 67.0%; Score 441; DB 1; Length 117; Best Local Similarity 84.5%; Pred. No. 1.8e-37; Matches 82; Conservative 3; Mismatches 12; Indels g δ

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Search completed: April 13, 2001, 15:40:18 Job time: 271 sec

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1 QVQLQQPGAELVKPGTSVKL......DGWDYAIDYWGQGTSVTVSS 121
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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09u191 homo sapien 09u188 homo sapien 09u184 homo sapien 09u173 homo sapien 09u173 homo sapien 09u173 homo sapien 09u174 homo sapien 091199 mus musculu 091199 mus musculu 091199 mus musculu 091199 mus musculu 09u196 homo sapien 09u196 homo sapien 075737 homo sapien 075738 homo sapien 075738 homo sapien 075728 homo sapien 075728 homo sapien 075728 homo sapien 075728 homo sapien	PRT; 117 AA. Created) Last sequence update) Last sequence update) Last annotation update) Last annotation update) .Cranlata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. Specht C., Koelsch E.; EMBL/GenBank/DDBJ databases. CDDE2AF84D499734 CRC64;	re 473; DB 11; Length 117; d. No. 4.2e-42; Mismatches 16; Indels 4; Gaps 1;
Q9UL91 Q9UL88 Q9UL71 Q9UL72 Q9UL72 Q9UL72 Q9UL74 Q9JUL74 Q9JUL96 Q9UUGP3 Q9UL96 Q9UL96 Q9UL96 Q9UL96 Q9UL96 Q75729 Q9UL75 Q75726 Q75726 Q75726 Q75728	भवाव प्रः	Score 47 Pred. No 10; Misma
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                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=DBA/2;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF206029; AAF69327.1; -.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNGCLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
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70.3%; Score 462.5; DB 11; Length 114;
Best Local Similarity 77.9%; Pred. No. 5e-41;
Matches 88; Conservative 7; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 LTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWD-YAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 110;
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12138 MW; ZEDE81FB5862C9AF CRC64;
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         110 AA
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         PRT;
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79.38;
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Best Local Similarity 79.3
Matches 88; Conservative
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         PRELIMINARY;
                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                             110 AA;
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Q9JL77
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Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., -Squinto S.P., Matis L.M., Evans M.J.;
Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2764 constant regions block human leukocyte binding to porcine endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NOKFKGKATLIVDKSSSTAYMQLNSLISEDSAVYCARDK----DYYFDYWGQGTTLIVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 458.5; DB 11; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.8%; Score 459; DB 11; Length 117; 72.7%; Pred. No. 1.2e-40;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ22311; CAB65236.1; -
INTERPRO; IPR003006; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13060 MW; D816AD0858A47E4C CRC64;
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                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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117 AA
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Best Local Similarity 72.73
Matches 88; Conservative
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  PRELIMINARY;
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SEQUENCE 117 AA; 13
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                                                                                                                                                                         Mus musculus (Mouse).
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Submitted (NOV-1996) to th
EMBL; U78799; AAD00291.1;
INTERPRO; IPR003006; -.
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Mueller J.P., Glannonl M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Matls L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
                                                                                                                                                                                            61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR---GGYDGWDYAIDYWGQGTSV 117
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                                                                                                    1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWWQWVKQRPGQGLEWIGAIYPGDGDTSY 60
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                         1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                               Indels
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71.8%; Pred. No. 1.4e-40;
tive 8; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.2%; Score 442.5; DB 1
76.1%; Pred. No. 5.8e-39;
Live 8; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Best Local Similarity 76.1<sup>s</sup>
Matches 86; Conservative
                             89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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109 AA;
    Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                            115 TVSS 118
                                                                                                                                                                                                                                                              118 TVSS 121
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NON_TER
SEQUENCE
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09JL75
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                         1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                4
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63.0%; Score 414.5; DB 4; Length 124;
Best Local Similarity 64.5%; Pred. No. 5.7e-36;
Matches 80; Conservative 17; Mismatches 24; Indels 3
                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                              24; Indels
the EMBL/GenBank/DDBJ databases.
                                                                                                                       4F65B193AFB77E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                     Score 437; DB 11;
Pred. No. 2.4e-38;
8; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
BERD: AR055022, AAD56258.1; -.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                               66.4%;
70.2%;
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                                                                                                                                                                                                                              85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDG-WDYAIDYWGQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TTEMBLRel. 15, Created)
01-0CT-2000 (TTEMBLRel. 15, Last sequence update)
01-0CT-2000 (TTEMBLRel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.7%; Score 412.5; DB 11; Length 110; 70.5%; Pred. No. 8e-36; Live 8; Mismatches 22; Indels 3;
                                                                                                                                                                  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                 62.9%; Score 414; DB 4; Length 119; 65.6%; Pred. No. 6.1e-36;
                                                                                                                                                                                                                                                                                                                                                         24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12052 MW; 84E6F2AD219AF95E CRC64;
                                                                                                                                                                                                                                                                                              13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD$5020; AAD$6256.1; -.
INTERPRO; IPRO03006; -.
PFAM; PF00047; 19; 1.
           119 AA
                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
           PRT;
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                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                         80; Conservative
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            PRELIMINARY;
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                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                \frac{119}{119} AA;
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110 AA;
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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NON_TER
SEQUENCE
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SEQUENCE
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Best focal 9
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                                                                                                                                                                                                           fetus."
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Gaps

focal Similarity 70.5 nes 79; Conservative

Matches

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STRAIN=BALB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                     61
                      2 ELVKPGASYKISCKASGYTFSNSWMWWYKLRPGQGLEWİGRIYPGDGDAYYNGKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNGELOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                        62 LTADKSSSTAYMQLSSLTSVDSAVYFCAR---SNWDVRFAYWGQGTLVTVSA 110
                                                                                 70 LTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.3%; Score 390; DB 4; Length 125;
60.0%; Pred. No. 2.1e-33;
live 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 AA; .13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , 2.1e-33;
ches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -.
INTERPRO; IPR003006; -.
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                                                                                                                                                                                                                                    PRT;
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MEDLINE=98277139; Pubmed=9614934;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.09
nes 75; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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NON_TER
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Q9JL85;
                                                                                                                                                                                       RESULT 11
Q9UL95
ID Q9UL95
AC Q9UL95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus."
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1 QVOLOQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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Best Local Similarity 55.4%
Matches 67; Conservative
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Best Local Similarity
Matches 69; Conserv
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                        OGUL89 PRELIMINARY; PRT; 116 AA.
09UL89;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
MAMMMALIA; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                            9 AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFK 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: |:| | |:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                        4,
                                                                                                                                                                                                                                                                                 69 TLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                           54.2%; Score 356.5; DB 4; Length 116; 60.3%; Pred. No. 6e-30; 1ve 16; Mismatches 29; Indels 1
                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MUZ., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                  Indels
                                                                DFE615FE6CED4EDE CRC64;
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Last annotation update)
                                                                                                                     Query Match 58.7%; Score 386; DB 11; Best Local Similarity 64.6%; Pred. No. 4.6e-33; Matches 73; Conservative 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035025; AAD56261.1; -.
INTERPRO; IPR003006; -.
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                                                             109 AA; 11944 MW;
EMBL; AF206021; AAF69319.1;
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Best Local Similarity 60.3%
Matches 70; Conservative
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01-MAY-2000 (TrEMBLrel, 1:
01-0CT-2000 (TrEMBLrel, 1:
CN 8 SCFV.
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                                                                                                             SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=SPLEEN;
shinobhara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-88332155; PubMed-9657749; Jacquemin M.G., Vander Elst L.P.L.; Mechanism and kinetics of factor VIII inactivation: study with an ING4 monoclonal antibody derived from a hemophilia A patient with inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinoh-BALB/C, Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 150 150
150 AA; 16031 MW; 563D164AB22802D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
IGG VH PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                             53.7%; Score 353.5; DB 55.4%; Pred. No. 4e-29; ive 16; Mismatches
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EMBL; AJ224083; CAA11829.1; -.
INTERPRO; IPR003006; -.
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20 QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY 79
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ARGGYDGWDYAIDYWGQGTSVTVS	
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSA	
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⁸⁰ AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDPD----AFDIWGQGTMVTVS 135

qq Qy Db

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Search completed: April 13, 2001, 15:39:52 Job time: $264\ \mathrm{sec}$

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¹²¹ S 121 | | | 136 S 136

PRASIL1 between HI SCFV PRASIO7 and p SCFV PRASIO8 and p SCFV PRASIO8 and p Fusion protein pNG Plasmid PNG4/55.18 Murine anti-CD18 A Lead binding MAD 8

R76088 W27122 R54756 R56482 R56483 W82743

520 520 517.5 517.

MAb 55.1 heavy cha MAb 55.1 heavy cha Murine antibody he

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1 QVQLQQPGAELVKPGTSVKL......DGWDYALDYWGQGTSVTVSS 121
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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ALIGNMENTS

RESULT

R22582 R56484 Y92156 R85495

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Sequence encoded b
Anti-hepatitis B h
Mouse-human chimae
Chimaric anti-hepatit
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Single chain antig
Anti-tobacco mosai
VH425 antibody hea
Scrvil B construct

R47493 W01578 W10584 W10584 W10539 W470239 W470239 W471054 W89535 R22583 R22583 R22583 R22583 R22583 R22584 R22583 R22584 R22586 R22587 R22587 R22587 R22587 R22587 R22587 R22587 R22587 R22588

\$111 \$110.5 \$10.5

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Mouse; Act-1 antibody; human alpha4-beta7 integrin; Madcsal adressin cell adhesion molecule-1; MadCAM-1; Musacosal adressin mrine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease. Murine Act-1 heavy chain variable region. /note= "signal peptide"
20..140
/note= "mature reco Location/Qualifiers 1..19 W53815 standard; Protein; 140 AA. 97WO-US13884 96us-0700737 (first entry) WO9806248-A2 06-AUG-1997; 15-AUG-1996; 14-JUL-1998 19-FEB-1998 Key Peptide Protein W53815; Mus sp W53815

(LEUK-) LEUKOSITE INC

Consensus protein Protein sequence o Heavy chain of a h Anti-DNA antibody Anti-EGFR antibody Anti-Fas MAD HFE7A

W53815 W53816 W53813 W07436 R79863 W83041 B14747

100.0 98.2 86.5 86.5 81.8 81.5 79.5 79.5 79.5

658 646 6466 523 523 523 523 523 523 523

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Murine Act-1 heavy

Mouse anti-Fas ant Murine anti-Fas an B-cell lymphoma CH Anti-EGFR antibody

R84555 R79861

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Misc-difference 7
                        Misc-difference
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Saldanha J;
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                                                                                                                                                                murine antibody Act-1. Act-1 is active against human alphat-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this paticular integrin. The Act-1 antibody inteferes with alphat-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used to inhibit the interaction of cells bearing alphat-beta7 with cells bearing alphat for alphat-beta7. It can be used for inhibiting leukocyte infilitration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKGKATLITVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                 20 qvqlqqpgaelvkpgtsvklsckgygytftsywmhwvkqrpgqglewigeidpsesntny 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus protein sequence of the murine variable heavy chain region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; Mumanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                        present sequence represents the heavy chain varaible region of
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                                                                           Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
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    Ringler DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "not specified, encoded by
                                                                                                                                                                                                                                                                                                                                                3, DB 19;
  Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                Score 658;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "not specified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "not specified,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "not specified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W53816 standard; Protein; 144 AA.
    Newman W,
                                                                                                                               Claim 27; Fig 9; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 121; Conservative
    Jones ST,
                                        WPI; 1998-159172/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                   N-PSDB; V20078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-1998
  Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 s 140
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                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W53816;
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The present sequence represents the consensus amino acid sequence comprising the variable region of murine Act-1 antibody determined from several independent mouse heavy chain variable region clones. Act-1 secretive against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCaM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCaM-1, which is present of high endothabial venules in mucosal lymph nodes. Variable regions were amplified from DNA encoding Act-1 using degenerate PCR primers V20079-88. The degeneracy of the PCR primers produced several different sequences, of which the present sequence is a consensus sequence. The present sequence was used to construct chimeric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGGGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 658; DB 19; Length 144; 100.0%; Pred. No. 3.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ringler DJ;
                                                          /note= "not specified, encoded by YTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "CDR3"
131..141
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "framework region
                                                                                                                                                                                                                                  "framework region
'note= "encoded by ATY"
                                                                                                                 /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                 "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 145pp; English.
                                                                                                                                                20..144
/note= "mature
                                                                                                                                                                                                                                                                                             "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                        "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       86..117
/note= "3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118..130
                                                                                                                                                                                                                                                                                                                                                                                69..85
/note= '
                                                                                                                                                                                                                                                                                                /note= '
55..68
                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LEUK-) LEUKOSITE INC.
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N-PSDB; V20085.
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20 qvqlqqpgaelvkpgtsvklsckgygytftsywmhwvkqrpgqglewigeidpsesntny 79 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVT 118

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Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The present sequence was used to construct chimeric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein sequence of murine variable heavy chain region of clone H2B#34.
                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
20 qvqlqqpgaelvkpgtsvklsckgygytftsywmhwvkqrpgqglewigeidpsesntny
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diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised immunoglobulin reactive with alpha-4-beta-7 used for treating inflammatory disease, pancreatitis, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newman W,
                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 2; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                       W53818 standard; Protein; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US13884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LEUK-) LEUKOSITE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9806248-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saldanha J;
                                                                                                                                                                                                                              140 s 140
                                                                                                                                                                      S 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                               W53818;
                                                                                                             80
                                                           61
                                                                                                                                                                      121
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The present sequence represents the heavy chain of humanised murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4 beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte Infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
Mouse; Act-1 antibody; human alpha4-beta7 integrin; Makscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrin
diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised immunoglobulin reactive with alpha-4-beta-7 used for treating inflammatory disease, pancreatitis, asthma, graft versus host disease and sarcoldosis
                                                                                                                                                                          Heavy chain of a humanised murine Act-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newman W, Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                    1..19
/note= "signal peptide"
20..180
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
                                                                                    W53813 standard; Protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Fig 11; 145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0700737.
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-159172/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V20076
                                                                                                                                                                                                                                                                                                            Mus sp.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9806248-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1996;
                                                                                                                                              14-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                 W53813;
             80
                                                                                                                                                                                                                                                                                                            Mus
                                                                                                                                                                                                                                                                                                                                                        Key
                                                         RESULT
                                                                        W5381
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Length 180;

Score 569; DB 19; Pred. No. 8.8e-40;

86.5%; 85.1%;

Query Match Best Local Similarity

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Gaps

; 0

Indels

Score 646; DB 19; Pred. No. 3.2e-46;); Mismatches 0;

98.2%; Scc. 100.0%; Pred

Query Match
Best Local Similarity 100.
Matches 118; Conservative

Length 137;

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61 ngkfkgkatltvdkssstaymqlssltsedsavyycakgrlry----famdywgrgtsyt 116
                                                                                                                                                                                                                                                                                                                                             NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-epidermal growth factor receptor (EGFR).single chain antibodies and antibodies constructed from anti-EGFR antibody fragments can be used for diagnosis of tumours and assessment of tumour growth in
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                 9
which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAD can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephrits and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.

The sequence was derived by aligning homologous anti-DNA MAD, whose sequences have been published, as well as several MAD of other specificities obtained from a database search.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain antibody; antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
                                                                                                                                                                                                                                                                                 1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-EGFR antibody heavy chain variable region (Clone L3 11D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-EGFR antibodies and single chain Fv antibody fragments obtained from phage-antibody libraries, useful for diagnosis
                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                     Score 538; DB 18; Length 1
Pred. No. 2e-37;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guessow D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosell E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blasco F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piulats J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R79863 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 53; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kettleborough AC, Mitjans F,
                                                                                                                                                                                                                       81.8%;
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94EP-0104160.
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-336972/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy of tumours
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                           119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T04016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERE ) MERCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9525167-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                            119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                         117 vss 119
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Best Local Sim
Matches 105;
                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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         0; Gaps
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                                   The present sequence is the heavy chain variable region of the group 9fll putative consensus anti-DNA monoclonal antibody (MAb),
                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain; variable region; anti-DNA; monoclonal; antibody; 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease; consensus; putative.
                                                                                                                                                                                                                                                                                                                                                                Anti-DNA antibody 9f11 group heavy chain variable region.
         Indels
         10;
         Mismatches
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/label= framework_III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/label= framework_I
                                                                                                                                                                                                                                                                         W07436 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= J_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR_III
         8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50..66
/label= CDR_II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31..35
/label= CDR_I
36..49
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                                                                                                                                                                                                                                                                                                                                      (first entry)
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           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swanson PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-011854/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T43805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9636361-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995;
                                                                                                                                                                                                                                                                                                                                      12-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996
           Matches 103;
                                                                                                                                                                s 121
                                                                                                                                                                                             s 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                       W07436;
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vitro and in vivo. They may also be used in a pharmaceutical composition for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. (See T04011-T04026 and
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWLGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                               HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; Systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; soleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                          Score 536; DB 16;
Pred. No. 3e-37;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..19
'label= Sig_peptide
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/label= Constant
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/note- "claim 9"
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118..128
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/label- CDR_H2
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/label- CDR_H1
                                                                                                                                                                                                                                                                                             81.5%;
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                                                                                                                                                                                                                                                                                                                                          Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0..140
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                              119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus,
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W83041
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This is the amino acid of the heavy chain of murine anti-human Fast chain was obtained from HFFA-secreting hybridoma (FERM BP-5828)

Chain was obtained from HFFA-secreting hybridoma (FERM BP-5828)

Chain was obtained from HFFA-secreting hybridoma (FERM BP-5828)

Chain was obtained from HFFA-secreting hybridoma (FERM BP-5828)

Chair bodies are capable of inducting apoptosis in abnormal cells antibodies are capable of inducting apoptosis in abnormal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, solderne, pernicious anaemia, Addison's disease, solderne, pernicious anaemia, Addison's disease, theumatoid arthritis, autoimmune haemolytic anaemia, scriitty, myasthenia carthritis, autoimmune haemolytic anaemia, scriitty, myasthenia ond insulin-dependent diabetes), allergles, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephitis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all clamed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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                                                                                                                                                                          Kimihisa I;
                                                                                                                                                                                                                                                                                                                                                            Reference Example 4; Page 187-188; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.5%; Score 523; DB 19;
83.5%; Pred. No. 1.4e-35;
                                                                                                                                                                     Hideyuki H, Hiroko Y, Jun O, Kir
O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse anti-Fas antibody HFE7A heavy chain.
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                                98AU-0059701
                                                                 97JP-0276064
                                                                                   97JP-0082953.
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Best Local Similarity 83.5
Matches 101; Conservative
                                                                                                                                      (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                       WPI; 1998-543440/47.
N-PSDB; V71029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 AA;
                                30-MAR-1998;
                                                                 08-OCT-1997;
                                                                                                   25-JUN-1997;
                                                                                                                                                                      Akio S, Hić
Masahiko O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 - NOV - 2000
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA.

To a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents the heavy chain of the murine anti-human Fas monoclonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
             Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKGKATLITVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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complementarity determining region; CDR; human Fas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 523; DB 21;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 67-68; 139pp; Japanese.
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83.5%;
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                                                                                                                                                                                                                                                                                              (SANY ) SANKYO CO LTD
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Best Local Similarity
Matches 101; Conserv
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                                                                                                               musculus
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                                                                                                                                                                                                                                                           30-SEP-1998;
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ingenue (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents comportations in cells with a normal system, by inhibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between the proposition of the invention have anti-inflammatory, anti-arenations are inflammatory, anti-arenations are inflammatory, anti-arenations are inflammatory, anti-arenatory dermatorogical, immunosupressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce compositions by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic complex erythematosus, Hashimotor disease, rheumatoid archititis, graft or versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral cells. They bind to both human and murine Fas, so can be evaluated in current entive ligand, do not induce ligand ecliver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents and murine antibody HFETA heavy chain described in the mative ligand, do not induce ligand ecliver disease, and have reduced risk of a murine antire native ligand.
             dermatological; immunosuppressive; thyromimetic; antitheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; nephrotropic; humanized; apoptosis; systemic luues erythematosus; HFSTA; Hashimoto disease; rheumatolod arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example reference 4; Page 100-102; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 523; DB 21;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.5%;
83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0276881.
98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-258930/23.
N-PSDB; A11546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA;
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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serizawa N,
                                                                                                                                                                                                                                                    Mus musculus
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Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;

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Single chain antibody, antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-EGFR antibodles and single chain Fv antibody fragments - obtained from phage-antibody libraries, useful for diagnosis and
                                                                                                                                                                                                 Anti-EGFR antibody heavy chain variable region (Clone L2 12B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Bendig MM, Blasco F,
Mitjans F, Piulats J,
                                             R79861 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 50; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94EP-0118970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy of tumours
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nes 99; Conserv
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                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1994;
17-MAR-1994;
                                                                                                                                               02-JUL-1996
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Best Local Si
Matches 99;
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11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic; B-cell lymphoma; CH12; IgM.
          NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYAIDYWGQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The heavy chain variable region amino acid sequence (given in R84554) of monoclonal antibody SCH94.03 shows extensive sequence similarity with the corresp. sequence (R84555) of the Igm produced by B-cell lymphoma CH12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases of the CNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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Pred. No. 5.7e-36;
4; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           B-cell lymphoma CH12 IgM heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 40; 63pp; English.
                                                                                                                                                                                                                                                                                         R84555 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.1%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0236520.
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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| 18 122
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                                                                                                               121 S 121
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Watches 9
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Anti-epidermal growth factor receptor (EGFR) single chain antibodies and antibodies constructed from anti-EGFR antibody fragments can be used for diagnosis of tumours and assessment of tumour growth in vitro and in vivo. They may also be used in a pharmaceutical composition for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. (See T04011-T04026 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OVOLQOPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 119;
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                                                                                                                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                                                                                       79.0%; Score 520; DB 16;
81.8%; Pred. No. 6.1e-36;
live 6; Mismatches 14
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ID R7
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MAD 55.1 (ECACC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, FV, scFV or V-min humanized 55.1 constructs have been expressed in myeloma cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding structure; complementarity determining region; CDR; colorectal cancer; tumor associated antigen; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
   call, colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAD; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen binding structures containing CDRs recognising the CA55 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                    Paterson DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine antibody heavy chain variable region consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%; Score 520; DB 16;
80.2%; Pred. No. 2.4e-35;
tive 10; Mismatches 14;
                                                                                                                                                                                                            97-98"
                                                                                                                                                                                                                                                                                                                                                                                                                    Hall SM,
                                                                                                                                                                                              /label= Mat_protein
/note= "claim 3, page
                                                                                                                               Location/Qualifiers
                                                                                                                                               1..19
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig.15; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                       93GB-0024819.
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                    DC, Boot C, 3, Wright AF;
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                                                                                                                                                                                                                                                                                                                                                                                      (ZENE ) ZENECA LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 97; Conserv
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03-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 qvqlqqpgaelvkpgasvqlsckasgytftgywihwvkqrpgqglewigevnpstgrsdy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An antigen binding structure is based on the CDRs (given in R76078-84) of the heavy (R76085) and light (R76086) chains of MAD 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CA55.1. It is optionally humanized and in the form F(ab')2, Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                               Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monochonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                         Paterson DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.0%; Score 520; DB 16; 80.2%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Hall SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 97-98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                       Copley CG,
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                                                                                                                                                                                                                                                                                                                          94GB-0011089.
93GB-0024819.
                                   21-NOV-1995 (first entry)
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Best Local Similarity 80.29
Matches 97; Conservative
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Wright AF;
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                                                                    55.1 heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 AA;
                                                                                                                                                                                                                                                                                                                          03-JUN-1994;
03-DEC-1993;
                                                                                                                                                                                                                                                                                          29-NOV-1994;
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Rose MS, Blakey

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Length 464; Indels us-08-700-737-9.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide sequence comprises a consensus sequence of murine heavy chain variable regions (VH) selected on the basis of identity to the VH region (see W27120) of monoclonal anti-idiotype antibody 11010. The sequences were obtained from a GenBank database search. A VL consensus (W27121) was also produced. 11010 has at least 18 departures from the consensus sequences (7 in the light chain and 11 in the heavy chain). B Occur within CDRs and 10 outside CDRs. 11010 polypeptides and polynucleotides can be used in vaccines and pharmaceutical compositions for the treatment of human milk fat globule-associated diseases such as breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours, especially breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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Pred. No. 8e-36;
5; Mismatches 14; Indels 3;
                                                                                                                                           /note= "complementarity determining region 2" 99..107
/label- CDR3
        Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine.
                                                                                                          "complementarity determining region 1"
                                                                                                                                                                                'note- "complementarity determining region 3"
                                                                                                                                                                                                                               /note= "unspecified amino acid residue"
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                                                                                                                     50..66
/label- CDR2
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95US-0575762.
96US-0591965.
                                                                                    31..35
/label= CDR1
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Best Local Similarity 81.8%;
Matches 99; Conservative
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                                                                                                                                                                                                                  Misc-difference 101
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                                                                                                                                                                                                                                                                                                                                                     13-DEC-1996;
20-DEC-1995;
26-JAN-1996;
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                                              Mus musculus
                                                                                                                                                                                                                                                                                                                               19-DEC-1996;
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Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus;
Penton fibre; Ad5; Fusion sites; PCR; polymerase chain reaction.
                                                                                                                          1..42
2.3.061= pelB leader peptide
23..142
/label- heavy chain variable region
                                                                                                                                                                                                                                                                  /label= (G4S)3 Linker
158. 269
/label= Light chain variable region
                                                                                                                /label= Single chain Fv fragment
                                            pRAS111 between HindIII and EcoRI sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
                                                                                                Location/Qualifiers
1..269
R54756 standard; Protein; 269 AA.
                                                                                                                                                                          VH CDR 1
                                                                                                                                                                                                                                                                                                                VL CDR 1
                                                                                                                                                                                                 72..88
/label- VH CDR 2
89..120
/label- VH FR3
                                                                                                                                                                                                                                    label- VH CDR
                                                                                                                                                                                                                                                                                                                                     208..215
/label- vt cDR
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                                                                                                                                                     23..51
/label- VH FR1
                                                                                                                                                                                  58..71
/label- VH FR2
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                                                                                                                                                                                                                                                                                                 'label- VL FR1
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/label- VL FR3
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                              (first entry)
                                                                                                                                                                                                                                                                                                        180..193
/label= V
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/label= 1
                                                                                                                                                                                                                                             132..142
                                                                                                                                                                                                                                                           143..265
                                                                                                                                                                                                                                                                                                                      194..207
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                                                                                                                                                                                                                                                                                                                                                    216..247
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                                                                                                                                                                                                                                                                                                                                                            /label
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N-PSDB; Q64817.
                             06-DEC-1994
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                                                                                 Synthetic.
                                                                                                        Protein
                                                                                                                       Peptide
                                                                                                                                      Protein
                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                           Protein
               R54756;
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R54756 showes an ScFv (VH and VL partner domains are linked via a flexible oligopeptide) between the HindIII and ECORI sites of pRASI11. The 130 bp HindIII-Pst fragment of pRASI11 (064806) was used to replace the corresponding fragment of pRASI11 (064817), to qenerate pRASI8 This generates a NIP-reactive SCFv (NIP = 4-hydroxyl-3-iodo-5-nitrophylacetic acid) with a BgIII cloning site immediately downstream of the pelB leader, suitable for inserting fragments of Ad5 fibre.
The invention is concerned with the fusion of an ScFv with the Ad5 fibre such that the fusion sequence can be used to target cells for
            Virus with modified binding moiety specific for the target cells - used to deliver genes for gene therapy and cancer treatment \,
                                                                                   Example 2; Page 69-70; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                       gene therapy.
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1; 1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60 Gaps Ţ; Query Match

Rest Local Similarity

18.6%; Score 517.5; DB 15; Length 269;

Best Local Similarity

81.8%; Pred. No. 2.2e-35;

Matches 99; Conservative 4; Mismatches 17; Indels 1; δλ

269 AA;

Sequence

61 NOKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120 23 qvqlqqpgaelvkpgasvklsckasgytftsywmhwvkqrpgrglewlgridpnsggtky 82 g ò g

121 S 121 οy

142 s 142

Search completed: April 13, 2001, 15:35:37 Job time: 116 sec

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140 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-801-500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-815A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07
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STREET:
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Sequence 2, Appli
Sequence 12328, A
Sequence 12328, A
Sequence 11339, A
Sequence 11223, A
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
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= 28, Appl
= 51, Appl
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4, Appli
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                                                                                                                        658
1 QVQLQQPGAELVKPGTSVKL.....DGWDYAIDYWGQGTSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 1, sequence 6, sequence 6, sequence 6, Sequence 7, Sequence 7, Sequence 28, Sequence 21, Sequence 51, Sequence 51,
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4: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-739-449-11638
US-09-386-658-4
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US-09-509-031-16
US-09-782-504-4
US-09-509-031-11
US-09-509-031-4
US-08-475-815A-7
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US-09-193-562D-28
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US-09-814-950-2
US-09-739-449-12328
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US-09-739-449-11939
US-09-739-449-11223
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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US-09-815-108-17
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                                                                                                                                                                                          7695 seqs, 1735856 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                              US-08-700-737-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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Maximum DB s
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                                          OM protein
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111
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Query Match
Best Local Similarity 47.99
Matches 58; Conservative
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US-09-782-504-4
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APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOLDES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                              61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                 20 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSY 79
                                  Gaps
                                                                1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGGGLEWIGEIDPSESNINY 60
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Score 486; DB 4; Length 140; pred. No. 1.8e-44; 8; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Erlanger, Bernard
APPLICANT: Erlanger, Bernard
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES.
FILE REFERENCE: 0575-54182/JPW/SHS/NVM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.7%; Score 426; DB 5; 67.8%; Pred. No. 2.6e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/509,031 CURRENT FILING DATE: 2000-06-09 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.00-509-031-16
Sequence 16, Application US/09509031
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09386658 GENERAL INFORMATION:
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        73.98;
76.98;
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                                         Conservative
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Best Local Similarity
Watches 82; Conserv
                      1 Similarity
93; Conserv
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          Query Match
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                                           Matches
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                                                                                                                                                                                                                                                                           59 NYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVT 118
                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence:ccMTLgL protein; OTHER INFORMATION: Sequence US-09-509-031-16
                                                                                                                                                                                           1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESNT 58
                                                                                                                                                        Gaps
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&
                                                                                                            Length 482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-U9-782-304-4
Sequence 4, Application US/09782504
Sequence 4, Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
Hellstrom, Karl Erik
Hellstrom, Karl Erik
Bruce, Kim Folger
Schreiber, George J.
Siegall, Clay
MCANGTEN Stephen
TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN
CARCINOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.8%; Score 242; DB 5; I
47.9%; Pred. No. 4.8e-19;
Live 24; Mismatches 31;
                                                                                                                  DB 5;
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NAME: ROSenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 840065.405D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                ; Score 278.5; DB 5; Pred. No. 1.9e-22; 27; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,504
FILING DATE: 12-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein sEQ ID NO: US-09-782-504-4
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                  Query Match 42.3%;
Best Local Similarity 43.9%;
Matches 54; Conservative 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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STATE: Washington
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SEQ ID NO 4
LENGTH: 495
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GENERAL INFORMATION:
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FROM TEACH TEACH TEACH
APPLICANT: Teaching M.
APPLICANT: Teaching M.
APPLICANT: Teaching M.
APPLICANT: Teaching M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATCHIN Ver. 2.1
                                                                                                                                                                               61 NOKFKCKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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APPLICANT: Suess, Garage M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tartinton, David M.
TILLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474.
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 342
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QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : OTHER INFORMATION: Description of Artificial Sequence: Kappa OTHER INFORMATION: protein sequence US-09-509-031-11
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16.3%; Score 107; DB 5;
Best Local SImilarity 27.3%; Pred. No. 2.4e-05;
Matches 35; Conservative 19; Mismatches 46
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US-09-509-031-6
; Sequence 6, Application US/09509031
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-509-031-11
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APPLICANT: Suess, Gabriele M.
APPLICANT: Tarilinton, David M.
APPLICANT: Tarilinton, David M.
APPLICANT: Tarilinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME CURRENT APPLICANTON NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                        53 PSESNTNYNOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 111
                                                                                                                                                                                                                                                                                                                                      2 VQLQQPGAELVKPGTSVKLSCKG-----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 PSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:TLHL protein: OTHER INFORMATION: sequence
                                                                                                                                                                                                                                            28;
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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Refef, Mitchell E.
APPLICANT: Refef, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
                                                                                                                                  Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
16.3%; Score 107; DB 5; Length 495;
Best Local Similarity 27.3%; Pred. No. 9.1e-05;
Matches 35; Conservative 19; Mismatches 46; Indels
                                                                                                                      16.3%; Score 107; DB 5; Length 34 27.3%; Pred. No. 5.9e-05; Live 19; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09509031; GENERAL INFORMATION: APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                   Query Match
Best Local Similarity 27.38
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     112 GQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                        134 GOGTKLEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| : :
GOGTKLEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 GQGTSVTV 119
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487 IQLESKGLTLQNSQWMNGTVIVDSTVGKDTLFLITW----TTQPPQILLW----535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 TNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AILPOPGELLADLAAKGFLVPLGDDTAKWVEENYGAGKSWVDLGSYKGKDGNKAY-FAFPF 155
                                                                                                                                                                                                                                                                                                                  -----QLSSLTSE---DSAVYYC---ARGGYDGW 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VQLQQPGAELVKP----GTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESN 57
                                                                                                                                                                                               9 AELUKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESNTNYNQKFKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT Pauli, Benedicht U.
APPLICANT Pauli, Benedicht U.
TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
FILE REFERENCE: 18617.0052
CURRENT APPLICATION NUMBER: US/09/193,562D
CURRENT FILING DATE: 1997-11-17
NUMBER OF SEO ID NOS: 47
ENCITH: 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 914;
                                                                                                                  Length 442;
                                                                                                               10.6%; Score 69.5; DB 5;
25.0%; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SMITHKLINE BEECHAM P.1.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GFDOOL18
CURRENT APPLICATION NUMBER: PCT/US01/09226
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR PRILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65.5; DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score v...,
25.0%; Pred. No. 3.5;
+ive 15; Mismatches
                                                                                                                           Ouery Match 10.6%; Score 69.5; D
Best Local Similarity 25.0%; Pred. No. 0.58
Matches 30; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US01-09226-51
Sequence 51, Application PC/TUS0109226
SERRAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09193562D GENERAL INFORMATION:
                                    ; ORGANISM: Agrobacterium tumefaciens US-09-739-449-9534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
                                                                                                                                                                                                                                                                                               67 KATLTVDISSSTAYM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-193-562D-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 TVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 TVTS 581
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-193-562D-28
LENGIH: 442
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)C
CURRENT FOLLIAG DATE: 2000-12-19
CURRENT FILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 9534
  RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 NYNQKFKGKATLTVDISSSTAY-MQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAEL-VKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLE-WIGEIDPSESNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.0%; Score 105; DB 4; Length 128; 27.0%; Pred. No. 3e-05;
                                                                                                                                                                                                                                           CALF: 2000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
                                                                                                               ADDRESSEE: PILLSBURY WINTHROP STREET: 1100 New York Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 3e-0
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23522-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030 REERRENCE/DOCKET NUMBER: 235 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
                                                      LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 128 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.0%
Best Local Similarity 27.0%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           TITLE OF INVENTION: RADI-
TITLE OF INVENTION: DIFF
TITLE OF INVENTION: LYMP
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-739-449-9534
                                                                                                                                                                                                                             20002
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                                                                                                                                                                  CITY: Wa
STATE: D
COUNTRY:
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Sequence 4, Application US/09814950
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO1174
CURRENT PAPLICATION NUMBER: US/09/814,950
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09814950
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEL, Ming-Hui et al
APPLICANT: WEL, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01174
CURRENT APPLICATION NUMBER: US/09/814,950
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                         56 SNTNYNQKFKGKATLTVDISSSTAY-MQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQG 114
                                                                                                                                                                                 Gaps
                                                                                     2 VQLQQPGAEL-VKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEID----PSE 55
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QLQQPGAELVKPGTSVKLSCKGYGYTFTSYWWHWVKQRPGQGLEWIGEIDPSESNTNYNQ 62
                                                            27;
                          Length 109;
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                                                        49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                          5,
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                    9.5%; Score 62.5; DB
23.2%; Pred. No. 0.6;
Live 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62.5; DB Pred. No. 1; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 KFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                 Query Match
Best Local Similarity 23.2%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 21.3
Matches 20; Conservative
                                                                                                                                                                                                                                 115 TSVTV 119
                                                                                                                                                                                                                                                                   102 TKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Human
US-09-814-950-2
                                                                                                                                                                                                                                                                                                                                         US-09-814-950-4
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US-09-814-950-2
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GENERAL INFORMATION:
APPLICANT: HINKLe, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT APPLICATION NUMBER: US/09/739,449
PRIOR PAPLICATION NUMBER: US/09/739,449
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
FEARMED OF 11638
                                                                                                                                                                                           3;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQPGAELVKPGT-----SVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 GYGYTFTSYWMHWVKQRPGGGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQL 83
                                                                                                                                                                                           16;
                                                                                                                                                 DB 1; Length 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 281;
                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09386658; GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard
APPLICANT: Chen, B1-Xind
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575-54182/JPW/SHS/MYM
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.7%; Score 64; DB 5;
25.8%; Pred. No. 1.3;
ative 17; Mismatches 3:
                                                                                                                                                                                   15; Mismatches
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                               9.9%; Score 65; 24.7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 SS----LTSEDSAVYYCA---RGGYDGWD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 SCSGTEQSVTECASRGWGNSDCTHD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Agrobacterium tumefaciens US-09-739-449-11638
                                                                                                                                                                                                                                                                                    52 DPS---ESNTNYNOKFKGKATLTVD 73
                                                                                                                                                           Similarity 24.79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.8%
Matches 23; Conservative
                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            US-09-739-449-11638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: mouse
US-09-386-658-4
                                                                                                                                        Query Match
Best Local Simi
Matches 21;
                                                                                 PCT-US01-09226-51
                                   753
                  SEQ ID NO 51
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Gaps

29;

Indels

36;

Length 172;

DB 5;

Score 62.5; DB Pred. No. 1; 9; Mismatches

ch 9.5%; 1 Similarity 21.3%; 20; Conservative

Best Local Similarity Matches 20; Conserv

Query Match

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April 13, 2001, 17:35:03 ; Search time 117.03 Seconds (without alignments) 166.311 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQQPGAELVKPGTSVKL......DGWDYAIDYWGQGTSVTVSS 121
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

9: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

15: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

16: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

16: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

17: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

21: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

22: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

23: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

23: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

24: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

25: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

26: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

27: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

27: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*

27: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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658
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                Run on:
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ALIGNMENTS

US-08-700-737-9

Sequence 9, Application US/08700737
GENERAL INFORMATION:
APPLICANT: Ponath, Paul D.
APPLICANT: Rigglar, Douglas J.
APPLICANT: Application Walter
APPLICANT: Newman, Walter
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
INUMBER OF SEQUENCES: 63 STREET: Hamilton, Brook, Smith & Reynolds, P.C. CITY: Lexington STATE: Massach... COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILLNG DATE: 15-40G-1996
CLASSIFICATION: 435 ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10 Massachusetts : USA CORRESPONDENCE ADDRESS: COUNTRY: Sequence 9, Appli Sequence 15, Appli Sequence 2, Appli Sequence 4, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 53, Appl Sequence 53, Appl Sequence 62, Appl 1 US-08-700-737-9 1 US-08-700-737-15 1 US-08-700-737-4 1 US-08-700-737-5 1 US-08-700-737-55 1 US-08-73-967-44 US-08-53-497-12 US-08-53-497-12 US-08-53-497-12

1000.0 1000.0 1000.0 98.2 86.9 86.9 81.5 79.8

9988,,,	sequence 48, Sequence 48, Sequence 48, Sequence 72, Sequence 3, Sequence 3, Sequence 9, Sequence 9, Sequence 7,	0 21125	adnence sdence sdence sedence sedence sedence sedence sedence sedence sedence sedence
14 18 10 11 11	11 US-08-766-350- 11 US-08-766-350A 12 US-08-816-455- 15 US-09-123-928- 17 US-09-313-928- 17 US-09-313-928- 17 US-09-313-928-	1 US-09-313-928 1 US-08-443-540-4 2 US-08-024-712-712-713-713-713-713-713-713-713-713-713-713	9 US-08-541-373 9 US-08-541-373 9 US-08-541-373 12 US-09-157-155 18 US-09-157-155 19 US-09-187-185 19 US-09-186-53 3 US-07-828-832 8 US-08-465-473 8 US-08-465-473
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			35 37 37 39 507 39 507 40 502.5 41 502.5 43 502.5 44 502.5

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TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 121; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6. CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY:
US-08-700-737-2
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                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                             APPLICANT: Porath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ones, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Baldanha, Jos
APPLICANT: Baldanha, Jos
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
ADDRESSED: ADDRESS:
                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                              Score 658; DB 11;
Pred. No. 7.2e-58;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUCRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08700737 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: V41/2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                 0;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  100.0%;
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TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22.5
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                                                                                                                                  ; TOPOLOGY: linear
US-08-700-737-9
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Best Local Similarity
                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                               Gaps
                                                                                         1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                     20 QVQLQOPGAELVKPGTSVKLSCKGYGYTFTSYWHHWVKQRPGQCLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Jones, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Saldanha, Jos
APPLICANT: Bendid, Mary M.
TITLE OF INVENTION: INTEGRIN
TITLE OF INVENTION: INTEGRIN
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Length 140;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  ; Score 658; DB 11;
; Pred. No. 8.6e-58;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGIGSTRATION NUMBER: 22,592
REFERENCE/CDOCKET NUMBER: LKS9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08700737 GENERAL INFORMATION:
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APPLICANT: Bendig, Mary M.

TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4

TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive

CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 121 amino acids
amino acid
                      Saldanha, Jos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 86.0
Matches 104; Conservative
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US-08-700-737-55
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80 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWQQGTSVIVS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Nowman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH \ 4 7
ITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH \ 4 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 137;
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                                                                                                                                                                                                                                                                                                                                                                                                      E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/700,737 FILING DATE: 15-AUG-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
98.2%; Score 646; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.3e-56;
Matches 118; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-640
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC: COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      Sequence 4, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ponath, Paul D.
Ringler, Douglas J.
Jones, S. Tarran
Newman, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-700-737-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                          140 S 140
                                      121 S 121
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY
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APPLICANT:
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/08700737

Sequence 19, Application US/08700737

GENERAL INFORMATION:
APPLICANT: Bonath, Paul D.
APPLICANT: Stock, Bouglas J.
APPLICANT: Application Walter
APPLICANT: Saldanha, Jos
APPLICANT: Allanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Massachneare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 121;
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                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: BLOOK DAVID E:
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1861-6240
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE (G17) 861-9540
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%; Score 572; DB
86.0%; Pred. No. 2.6e-
Live 7; Mismatches
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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61 NOKFKGKATLITVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                            61 NEKFRRATLIYODKSSSTVYMQLSSLTSEDSAVYYCARSG--GFYYGMDYWGGGTSVIVS 118
                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                                                                                                                                                                                                                                                                                     ;
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TITLE OF INVENTION: Anti-EGFR Single-Chain Fvs and Anti-EGFR
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCE: 32
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
                                                                                                                                                                                                                                                      Length 119;
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APPLICATION NUMBER: US/08/553,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%; Score 536; DB 9;
85.1%; Pred. No. 9.7e-46;
tive 4; Mismatches 12;
                                                                                                                                                                                                                                                          81.5%; Score 536; DB 4; ilarity 84.3%; Pred. No. 9.7e-46; Conservative 5; Mismatches 12
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/050001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-553-497-12
Sequence 12, Application US/08553497
SERVERAL INFORMATION:
               REFERENCE/DOCKET NUMBER: 00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 12:
                                                                                                              44:
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TYPE: amino acid
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                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                     LENGTH:
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                                                               MEDIUM TIFE: FILPLY GESTER

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737

FILING DATE: 15-AUG-1996

CLASSIFICATION: 435

ATTORNEY/AGBNT INFORMATION:
NAME: BTOOK, David E.
REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LKS95-10

TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 861-6240

TELEFAX: (617) 861-6540

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Syamal K. Datta
APPLICANT: Syamal K. Datta
TITLE OF INVENTION: METHODS FOR INHIBITING THE
TITLE OF INVENTION: ACTIVITY OF PATHOGENIC T
TITLE OF INVENTION: HELPER CELLS ASSOCIATED WITH
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMBUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordOPErfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 572; DB 11;
Pred. No. 4.1e-49;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/764,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/08073967
GENERAL INFORMATION:
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225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.9%;
86.0%;
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TYPE: amino acid
TOPOLOGY: 1:-
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                                                     Floppy disk
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Best Local Similarity 86.0
Matches 104; Conservative
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                 ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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ZIP: 02110-2804
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STREET: 222
TMV: Boston
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.6%; Score 524; DB 8; Length 119
83.7%; Pred. No. 1.5e-44;
Live 5; Mismatches 9; Indels
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,540
FILING DATE: US/08/443,540
FILING DATE: US/08/443,540
ATTORNEY/AGENT INFORMATION:
NAME: KOGSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 30344-21107.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ. ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GREENICANT: SCRIZAWA, NOBUGUSA
APPLICANT: ICHIKAWA, Kimihisa
APPLICANT: Ohtsuri, Jun
APPLICANT: Ohtsuri, Jun
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Ario
APPLICANT: Shiraishi, Akio
APPLICANT: Yoshida, Hiroko
APPLICANT: Yoshida, Akio
APPLICANT: Yoshida, Akio
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126/HG
CURRENT FILING DATE: 1998-04-01
EARLIER APPLICATION NUMBER: JP HEI 9-16908B
EARLIER FILING DATE: 1997-04-01
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09053583A; GENERAL INFORMATION:
755 Page Mill Road
                                                                     ZIF: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.6
Best Local Similarity 83.7
Matches 103; Conservative
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                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                         Palo Alto
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US-08-443-540-62
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                                                                                                               APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Sunder, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HIPPEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: AMBLILON, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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Pred. No. 1.3e-44;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
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; Sequence 62, Application US/08443540
; GENERAL INFORMATION:
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MOITISON & FOEISET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-1996
15-AUG-1996
18-AUG-1996
18-AUG-1996
                                                                        Sequence 53, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BEOCK. DAVID E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95
TELECHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.8%;
Similarity 79.5%;
11; Conservative
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|||||
| 121 TTVTVSS 127
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US-08-700-737-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 101;
                                                 US-08-700-737-53
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5

Gaps

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Length 119;

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TITLE OF INVENTION: Anti-Fas Antibodies FILE REFERENCE: 980126CIP/HG
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                                                                                                                                               464
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                                                                                                                                                                Gaps
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                                                                                                                                                                                                                  20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNY 79
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                                                                                                                           Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.5%; Score 523; DB 18; Length 464; 83.5%; Pred. No. 9.5e-44; iive 4; Mismatches 16; Indels
                                                                                                                                                              Indels
                                                                                                                         79.5%; Score 523; DB 14;
83.5%; Pred. No. 9.5e-44;
                                                                                                                                           Pred. No. 9.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/408,646A CURRENT FILING DATE: 1999-09-30 BARLIER APPLICATION NUMBER: JP 10-276881 EARLIER FILING DATE: 1998-09-30 NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REPERENCE: 990340/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-499-662-9
Sequence 9, Application US/09499662
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09408646A GENERAL INFORMATION:
                                                                                                                                          Best Local Similarity 83.5
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                  ; ORGANISM: Mus musculus US-09-053-583-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-408-646-9
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Best Local Similarity
Matches 101; Conserv
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US-09-408-646-9
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SEQ ID NO 9
                                   TYPE: PRT
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                    LENGTH:
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Sequence 28, Application US/08692084
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Asskura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION USING MON
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            ö
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
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COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 08-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                             Score 523; DB 18;
Pred. No. 9.5e-44;
4; Mismatches 16;
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FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/09/499,662
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: US 09/053,583
EARLIER FILING DATE: 1998-04-01
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26,742
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             Query Match 79.5%;
Best Local Similarity 83.5%;
Matches 101; Conservative 4
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MEDIUM TYPE: Floppy
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-779-784-28

Sequence 28, Application US/08779784

Sequence 28, Application US/08779784

GENERAL INFORMATION:

APPLICANT: Miller, David J.

APPLICANT: Asakura, Kunihiko

TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
                                                              DB 10; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DE-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION NUMBER: US/08/79,784
PRIOR APPLICATION NUMBER: US/08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US/08/520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 26,742
RELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEEPA: 201-487-5800
TELEGRAM: 122 amino acids
LYYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
                                                          Score 520.5; DB 1
Pred. No. 3.5e-44;
4; Mismatches 18
                                                            79.1%;
81.1%;
                                                            Query Match
Best Local Similarity 81.19
Matches 99; Conservative
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US-08-692-084-28
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Query Match
Post Local Similarity 81.1%; Pred. No. 3.5e-44;
Matches 99; Conservative 4; Mismatches 18; Indels 1;

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Appl Appli

Seguence Sequence Seq

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GENERAL INFORMATION:
APPLICANT: RETLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ADAN: JAUME
APPLICANT: ADAN: JAUME
APPLICANT: ROSELL, ELISABET
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: BLASCO, FRANCESC
APPLICANT: BLASCO, FRANCESC
APPLICANT: BLASCO, ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTI-BODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEF: MITLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
COUNTY: US
COUNTY: US
COUNTY: US
CIP: ARLINGTON
COUNTY: US
COUNTY: US
APPER-
MPTIMP: 22201
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
CLASSIEFCATION: 30.0
PILING DATE: 17 NOV-1995
CLASSIEFCATION: 30.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16 AMR-1995
FILING DATE: 16 AMR-1995
FILING DATE: 17 NAR-1994
FILING DATE: 17 NAR-1994
FILING DATE: 17 NAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 17 NAR-1994
ATTORNEY/AGENT INPOMMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION UNMBER: 33,302
REGISTRATION NUMBER: 33,302
  US-08-894-922A-14
US-08-894-922A-14
US-08-894-922A-10
US-09-881-037-16
US-09-065-059-5
US-08-737-560A-10
PCT-US93-11611-4
US-08-553-497A-22
US-08-11-202-1
US-08-11-202-1
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US-08-655-57
US-08-810-037-17
US-08-881-037-15
US-08-881-037-15
US-08-881-037-15
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US-08-481-181-78
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
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Patent No. 5844093
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TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
  RESULT 1
US-08-553-497A-12
  288
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                                                                                                                    April 13, 2001, 15:34:02; Search time 28.17 Seconds (without alignments) 82.517 Million cell updates/sec
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Sequence 62, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 33, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 61, Appli
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658
1 QVQLQQPGAELVKPGTSVKL.....DGWDYAIDYWGQGTSVTVSS 121
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Sequence 16,
Sequence 14,
Sequence 20,
Sequence 24,
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Sequence 11,
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'Cgn2_6/ptodata/2/laa/5A_COMB.pep:*

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'Cgn2_6/ptodata/2/laa/5A_COMB.pep:*

'Cgn2_6/ptodata/2/laa/6A_COMB.pep:*

'Cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

'Cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-8B1-037-62
US-08-557-620-9
US-08-553-497A-8
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US-08-491-988-7
US-08-881-037-61
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US-08-881-124
US-08-235-838-11
US-08-465-473B-11
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Maximum Match 100%
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Match Length
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Maximum DB seq
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Perfect score:
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                                                                                                                      Run on:
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Gaps

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61 NOKFKCKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYAIDYWGQGTSVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
                                                                                                      1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNINY 60
                                          9
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                                                                                                                                                                                                                                                                                                           APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C. STREET: Two Militia Drive STREET: Lexington STRTE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATE: US/08/236,520
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 520.5; DB 1;
Pred. No. 9e-41;
4; Mismatches 18;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MMY92-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                Sequence 9, Application US/08236520; Patent No. 5591629; GENERAL INFORMATION:
    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.1%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TOPOLOGY: ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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      Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                                     Length 119;
                                                                                                                                     81.5%; Score 536; DB 2; Length 11 ilarity 85.1%; Pred. No. 3.4e-42; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 524; DB 3;
Pred. No. 4.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 203442110710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MXY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Konski, Antoinette F. REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 494-0792
                  SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                           Best_Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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61 NOKFKGKATLÍVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 520; DB 2; Length 119; 81.8%; Pred. No. 9.8e-41; 1.1ve 6; Mismatches 14; Indels
                                                                                                                                     ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD. SUITE 1400 STATE: VA COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/53,497A
FILING DATE: 17-NOV-1995
CLASSICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: MERCK 1726
TELECOMMUNICATION NUMBER: MERCK 1726
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION;
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TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIGLATS, JAUME
TITLE OF INVENTION: ANTI-EG
TITLE OF INVENTION: ANTIBOD
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
       BLASCO, FRANCESC
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 119 amino acids
amino acid :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-553-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 99; Conserva
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US-08-353-400-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 122;
                                                                                           APPLICANT: Mayo Foundation for Medical Education Research TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REWYELINATION NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.1%; Score 520.5; DB 5; Length Best Local Similarity 81.1%; Pred. No. 9e-41; Matches 99; Conservative 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILLIG DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAY92-01 PCT
TELECOMMUNICATION INFORMATION:
TELEFAN: 617-861-6240
                                                 Sequence 9, Application PC/TUS9505262 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08553497A Patent No. 5844093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BENDIG, MARY M.
ANSELL, KEITH H.
GUSSOW, DETLEF
ADAN, JAUME
MITJANS, FRANSESC
ROSELL, ELISABET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KETTLEBOROUGH, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 122 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                             CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein PCT-US95-05262-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KETTLEBO
APPLICANT: BENDIG,
APPLICANT: GUSSOW,
APPLICANT: ADAN, JA
APPLICANT: MITJANS,
APPLICANT: ROSELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
         RESULT 4
PCT-US95-05262-9
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       RESULT
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RESULT 9
US-08-491-988-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%; Score 520; DB 1; Length 445; 80.2%; Pred. No. 4.3e-40;
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APPLICATION NUMBER: US/08/353,400
CUMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS SOFTWARE: Patentin Rolease #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/353,400 FILLING DATS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DAYE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SI, OUENCES: 37
COMPUTER RELDABLE FORM:
MEDIUM TYIE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9411089.7
FILLING DATS: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 33:
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amino acid
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.0%
Best Local Similarity 80.2%
Matches 97; Conservative
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MOLECULE TYPE: protein

US-08-353-400-36
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYP3: protein US-08-353-400-33
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                                                                       1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
                                                                                           20 QVQLQQPGAELVKPGASVQLSCKASGYTFTGYWIHWVKQRPGGCLEWIGEVNPSTGRSDY 79
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79.0%; Score 520; DB 1; Length 464; 80.2%; Pred. No. 4.5e-40; ive 10; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 517.5; DB 2
Pred. No. 4.1e-40;
4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/428,257A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08491988 Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Jules E. Goldberg
261 Madison Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS:
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81.8%;
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amino acid
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Best Local Similarity 81.89
Matches 99; Conservative
                                           97; Conservative
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10016-2391
       Query Match
Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07 CLASSIFICATION:
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1:0, Version #1.25
SOFTWARE: PatentIn Release #1:0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,908
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
WOMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                           18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             CARACTE TELEGRATION NUMBER: US/08/491, FILING DATE: 18-DEC-1995 CLASSIFICATION: 424 ATTORREYAGENT INRORMATION: NAME: COLDBERG, ULLES E. RELECOMMUNICATION NUMBER: 24,408 TELEFONE: 212-986-4090 TELEFAX: 212-986-4090 TELEFA
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Best Local Similarity 81.8%;
Matches 99; Conservative
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amino acid
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LENGTH: 415 amino acid
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INFORMATION FOR SEQ ID NO:
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; MOLECULE TYPE: protein
US-08-491-988-9
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US-08-491-988-7
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STATE:
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STREET: 261 MADISON AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                        ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
STREET: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 1001b-6234
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: IB-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24.408
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.6%; Score 517.5; DB 2; 81.8%; Pred. No. 4.1e-40;
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APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
ITILE OF INVENTION: Compounds for targeting
WHBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                   APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 269 amino acids TYPE: amino acid
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APPLICANT:
                                          APPLICANT:
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78.6%; Score 517; DB 3; Length 119; 82.1%; Pred. No. 1.8e-40;
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                                                                                                                                                                                                                                                                        Sequence 61, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
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STREET: 755 Page Mill Road
CITY: Palo Alto
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TELEX:
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amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Best Local Similarity
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US-08-881-037-63
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                                                                                  S 121
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ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 517.5; DB 2;
Pred. No. 7.1e-40;
4; Mismatches 17;
                                                                                                                                                                       Score 517.5; DB 2
Pred. No. 6.7e-40;
4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: EPERFICS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: EDGNARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/491,988
18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08491988 Patent No. 5973116
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NAME: GOLDBERG, JULES E.
REGISTRATICN NUMBER: 24,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 212-986-4090 TELEFAX: 212-818-9479
                                                                                                                                                                       78.6%;
81.8%;
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81.8%;
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LENGTH: 435 amino acids
TYPE: amino acid
                                                                                                                                                              Query Match 18.0%
Best Local Similarity 81.8%
Matches 99, Conservative
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Best Local Similarity 81.8 Matches 99; Conservative
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                                               , MOLECULE TYPE: protein US-08-491-988-7
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  amino acid
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                                TOPOLOGY:
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US-08-491-988-5
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61 NQKFKGKATLIVDKSSSTAYMQLSSLTSEDSAVYYCAKGRLRY----FAMDYWGQGTSVT 116
                                                                                                                         61 NQKFKGKATLITVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
                                    1 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 60
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Search completed: April 13, 2001, 15:36:09 Job time: 127 sec
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Pred. No. 2.3e-40;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                     COUNTY: USA

ZIP: 94304-1018

COUNTY: USA

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible .

OBFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAECHIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/881,037

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/443,540

FILING DATE: 18-MAY.1995

CLASSIFICATION: 530

ATPONEY/AGENT INPORMATION:

NAME: KONSK1, AALOIDELEE F

REGISTRATION NUMBER: 34,202

REERERENCE/DOCKET NUMBER: 34,202

REERERENCE/DOCKET NUMBER: 34,202

RELEFAK: (650) 813-5600

TELLEFAK: (650) 494-0792
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Sequence 60, Application US/08881037

Sequence 60, Application US/08881037

Settent No. 6080588

GENERATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
Sequence 63, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: G14ck, Gary D.
TITLE OF INFORMATION: Patrick C.
TITLE OF INFORMATION: DNA BINDING ANTIBODIES
WUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                          ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
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STREET: 755 Page Mill Road
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SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 82.1%;
Matches 101; Conservative 6
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STATE: C.
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61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG--GYDGWDYAIDYWGQGTSVT 118
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                                                                                                                                                                                               COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
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Pred. No. 4.2e-40;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%;
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LENGTH: 119 amino acids
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Best Local Similarity 81.3°
Matches 100; Conservative
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STATE: CASTONIANTE: USACOUNTRY: Usacountry
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein . protein search, using sw model

April 13, 2001, 15:36:46; Search time 32.39 Seconds (without alignments) 280.069 Million cell updates/sec Run on:

US-08-700-737-12 695 1 MKLPVRLLVLLLFWIPVSGG.......CLQGTHQPYTFGGGTKLEIK 132 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

198801 seqs, 68722935 residues Searched:

198801 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RIES	scri	Caronic according T	kanna chain	ka pro	400	light chain	kanna chain	To kanna chain pre	i-DNA autoan	Id kanna chain nre	Id kappa chain bro	Ta kanna chain na	anti-diadyth trans	To kanna chain neo	y Auppa	y happa chain	y kappa chain	y vappa		y kappa chain	y vappa chatii	y vappa	y warpa chain v	toppe chair	LY NAPPA CHAIN	To be a control of	TA PART CHAIN	To hear the training	To here the	ממא ענו ממא מד	y nappa ciiai
SUMMARIES	QI	25	н30560	E30560	S37203	B39276	B34904	C34904	PL0202	B32513	B30577	D34904	PH0106	D29380	PS0074	634903	809259	552449	PT0178	C29380	523230	A49032	S22902	\$24503	542611	524536	KZHIIRP	25452	27.0	\$24500	
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æ	Ouery	٠.						79.1						77.6					75.3			71.6								70.3	
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cha1n	kappa chain	kappa chain	kappa chain	kappa chain	kanna chain	kappa chain	kanna chain	kanna chata	TONA CHATA	kanna chata	1 4	happa Chall	Cuatu	chain	chain	Ig kappa chain v r
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488	1 00	407.0	487.5	486	486	484	484	483	483	481.5	481.5	481	107	T 1	480.5	480
30	1 6	7 (33	34	32	36	37	38	33	40	41	42	6 1	2 :	44	45

ALIGNMENTS

RESULT

B25912 Ig kappa chain precursor V region (W3129) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000 C;Accession: B25912 C;Accessi	A; Molecule type: mRNA A; Residues: 1-132 <bor> A; Cross-references: GB:M15874; NID:g196839; PIDN:AAA38796.1; PID:g196840 A; Note: the authors translated the codon CTC for residue 120 as Ser C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence (fragment) #status predicted <sig> F; 20-132/Product: Ig kappa chain V region W3129 #status predicted <var> F; 35-114/Domain: immunoglobulin homology <imm></imm></var></sig></bor>
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Gaps ö Query Match 89.2%; Score 620; DB 2; Length 132; Best Local Similarity 90.8%; Pred. No. 2.3e-47; Matches 118; Conservative 4; Mismatches 8; Indels

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123 FGGGTKLEIK 132 ò gg

RESULT 2
H305CD chain V region (36.1.2D) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: H30560
R; Matr-1889 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C; Accession: H30560
R; Matsuda, T.; Kabat, E.A.
J: Immunol. 142, 863-870, 1989
A; Titje: Variable region cDNA sequences and antigen binding specificity of mouse mono

A;Reference number: A30560; MUID:89110062 A;Accession: H30560 A;Status: preliminary

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0;

Indels

Length 112,

; DB 2; Lev. 1.8e-42;

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R; Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A; Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis
A; Reference number: A39276; MUID:91088540
A; Accession: B39276
                                                                                                                                                                                                                                                                                                                                                                 Ig light chain precursor V-D-J region (6-19) - mouse C; Species: Mus musculus (house mouse) C; Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000 C; Accession: B39276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-131 <-REL>
A;Cross-references: GB:M55313; NID:g198095; PIDN:AAA63385.1; PID:g198096
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
                                                                                                            DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF
                                                                                                                                         SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                               80.6%; Score 560.5; DB 2
80.3%; Pred. No. 3.5e-42;
iive 10; Mismatches 15
                                                                        Mismatches
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                        Score 563;
Pred. No. 1.
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94.6%;
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Best Local Similarity
Matches 106; Conserv
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A; Residues: 1-131 <BED>
                                                    Similarity
                                                                          106;
                               Query Match
                                                       Local
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Matches
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C;Species: Mus musculus (house mouse)
C;Species: 33-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000
C;Date: 23-Mar-1989
C;Accession: E30540
R;Matsuda, T: Kalat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monocle
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A;Description: Production and cloning of TWV-specific monoclonal antibodies. A;Reference number: S37200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-112 <FEIS>
A;Cross-references: EMBL:X74588; NID:9402597; PIDN:CAA52665.1; PID:91333980
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-113 <MAT>
A; Cross.references: GB: M24275; NID:g197085; PIDN:AAA63372.1; PID:g197086
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterctetramer; immunoglobulin
F; 16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                          Score 576; DB 2; Length 11 Pred. No. 1.3e-43; 0; Mismatches 3; Indels
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Pred. No. 2e-43;
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A; Accession: E305:0
A; Status: preliminary
A; Molecule type: IRNA
A; Residues: 1-113 < MATA.
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Best Local Similarity 97.3%;
Matches 109; Conservative
                                                                                                                                                                          Query Match 82.9%;
Best Local Similarity 97.3%;
Matches 109; Conservative
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Length 131;

DB 2;

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A;Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589.1; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-114/Domain: immunoglobulin homology <IMM>
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YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                   Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Bedayk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W. J. Biol. Chem. 265, 133-138, 1990
A.Title: Active site structure and antigen binding properties of A.Title: Active site structure, MUD:90094387
A.Reference number: A34903; MUID:90094387
A.Scession: B34904
A.Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor V region (12-40 and 5-14) - mouse C;Species: Mus musculus (house mouse) C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change C;Accession: B34904; H34903
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Best Local Similarity 94.77
Matches 107; Conservative
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A; Residues: 1-131 <BED>
B; Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
B; Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
A; Title: Comparison of variable region primary structures within an anti-fluorescein idi
A; A; Accession: 131485
A; A; Accession: 131485
A; Status: preliminary
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-DNA autoantibody BV16-13, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decession: PL0202
R;Smitch, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1998
A;Telle: Variable region primary structures of monoclonal anti-DNA autoantibodies from A;Reference number: PL0198; MUID:90309768
A;Nolecule type: mRNA
A;Residues: 1-114 <SMI>
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                                                                                                                  61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                         1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
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A;Molecule type: protein
A;Residues: 20-52 <BE2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary; not compared with conceptual translation
                  Indels
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   1.4e-41;
ches 16;
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Pred. No. 3.2e-41;
); Mismatches 17
    ed. No. 1.46
Mismatches
    Pred.
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79.5%; Pred
9; F
 80.38;
               106; Conservative
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Similarity
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Best Local Similarity
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Best Local
Matches 10
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A;Title: Generatic elements used for a murine lupus anti-DNA autoantibody are closely r A;Reference number: A30577; MUID:85159423
A;Accession: B30577
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C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 21-Jan-2000
C;Accession: B30577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:X53642; NID:950192; PIDN:CAA37693.1; PID:9930138 C$Superfamily: immunoglobulin V region; immunoglobulin homology cimps F:16-95/Domain: immunoglobulin homology cimps F:24-39/Region: complementarity-determining 1 F:55-67/Region: complementarity-determining 2 F:55-67/Region: complementarity-determining 2 F:95-103/Region: complementarity-determining 3 F:102-114/Region: JH region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
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A;Residues: 1-131 <KOF>
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Pred. No. 5.9e-41;
8; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 548.5; DB 2
Pred. No. 3.4e-41;
1; Mismatches 4
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94.78;
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Best Local Similarity 79.5%;
Matches 105; Conservative
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F;35-114/Domain: immunoglobulin homology <IMM>

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ig kappa chain V region (38C13.V7) - mouse
C; Species: Mus musculus (house mouse)
C; Species: J1-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C; Accession: PS0074
R; Levy, S.; Campbell, M.J.; Levy, R.
A; Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrang A; Reference number: A92781; MUID:89310348
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C;Accession: D29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the A;Reference number: A92612; MUID:88007582
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                                                                                  Length 132;
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Pred. No. 2.6e-40;
8; Mismatches 18; Indels
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A; Residues: 1-111 <LEV>
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-131 <CHE>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin
F;34-113/Domain: immunoglobulin homology <IMM>
                                                                                                                                                         Indels
                                                                                     DB 2;
                                                                                                                                                     17;
                                                                                     Score 540.5; DB Pred. No. 2e-40;
                                                                                                                                                         9; Mismatches
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Best Local Similarity 78.8%;
Matches 104; Conservative
                                                                                     77.8%;
ilarity 79.5%;
Conservative
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A; Status: translation not shown
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                                                                                            Query Match
Best Local Similarity
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R:Bedzyk, W.D.; Hurron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
R:Bedzyk, W.D.; Hurron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
B. Biol. Chem. 265; 133-138, 1990
A;Title: Active s:te structure and antigen binding properties of idiotypically cross-rea A;Reference numbe:: A34903; MUID:90094387
A;Accession: D34914
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nRNA
A;Residues: 1-131 ABDDA
A;Residues: 1-131 ABDA
A;Residues: 1-131 AB
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A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chair A;Reference number: PH0105; MUID:91015092
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C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C;Accession: PH0106
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C;Species: Mus mu:culus (house mouse)
C;Date: 27-Jul-19:0 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
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A;Moleocule type: nRNA
A;Residues: 1-132 <nRn>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                              Score 546.5; DB 2;
Pred, No. 5.9e-41;
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                                                                                                                                                                                                           9; Mismatches
C;Keywords: heterctetramer; immunoglobulin F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                   78.6%;
|Jarity 79.5%;
|Conservative
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Cincession: G34903
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Blol. Chem. 255, 133-138, 1990
A; Title: Active site structure and antigen binding properties of idiotypically cross-rea A; Reference number: A34903; MuID: 90094387
A; Accession: G34903
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Status: G34903; MuID: 90034387
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
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                                                                                                                                                                                                  21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
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          Length 111;
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Best Local Similarity 78.0%; Pred. No. 3.6e-40;
Matches 103; Conservative 9; Mismatches 19; Indels
                                                                                                      Indels
Score 537.5; DB 2;
Pred. No. 3e-40;
1; Mismatches 6;
77.38;
Query Match 77.3'
Best Local Similarity 92.9'
Matches 104; Conservative
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OM protein - protein search, using sw model

April 13, 2001, 15:40:18 ; Search time 21.32 Seconds (without alignments) 212.088 Million cell updates/sec Run on:

US-08-700-737-12 695 1 MKLPVRLLVLLEFWIPVSGG.......CLQGTHQPYTFGGGTKLEIK 132 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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FQQRPGQ::PRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGYYYCMQGTHWS 120
                                                                                                                                                                                                                          Novotny J., Margolies M.N.;
Novotny J., Margolies M.N.;
Novotny J., Margolies M.N.;
Manino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Biochemistry 22:1153-1158(1983).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT BINDS DIGOXIN.
PIR; A01914; KVMS26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Aetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eitheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=1606;
                                                                                                                                                        Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eu.ihezia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=1090;
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Pred. No. 2.9e-40;
8; Mismatches 14; Indels
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COMPLEMENTARITY-DETERMINING 1.
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COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                Immunoglobulin V region; Monoclonal antibody; Hybridoma.
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15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                          12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                               21-JUL-1986 [Rel. 01, Created)
21-JUL-1986 [Rel. 01, Last sequence update)
15-JUL-1999 [Rel. 38, Last annotation update)
1G KAPPA CHAIN V-II REGION 26-10.
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(Rel. 06, Last sequ
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                               121 YTFGGGTHLEIK 132
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121 WTFGQGT!:VEIK 132
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SEQUENCE FROM N.A.
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01-JAN-1988 (
15-JUL-1999 (
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P06309;
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Best Local Simi
Matches 90;
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KV2G_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 NRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klobeck H.G., Solomon A., Zachau H.G.; "Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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COMPLEMENTARITY-DETERMINING
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Pred. No. 2.2e-35;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION TEW.
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MEDLINE-74148480; PubMed-4596149;
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MEDLINE=84191506; PubMed=6325927;
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Immunoglobulin V region; Signal.
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nilarity 71.3%; l
Conservative 11;
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P01617;
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KV2B_HUMAN
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P18135;
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       MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH UPLASMA CELL DYSCRASIA AND AMYLOIDOSTS.

MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                              21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-I- MISCELLANEOUS: PHIS IS A BENCE-JONES PROTEIN.
PIR; A01885; KZHUCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-II REGION CUM.
Homo saplens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
MCBL_Taxib=9606;
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                                                                                                                                      COMPLEMENTARITY - DETERMINING FRAMEWORK 3.
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                                                                                                  protein; Amyloid.
                                                                                                                                                                                               0C3C38F81F1843CA CRC64;
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                                                                                                                                                                                                                           ; Score 418; DB 1;
; Pred. No. 5.4e-35;
15; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interracy 17, 19; 1,
Immunoglobulin V region; Bence-Jones protein.
95 BY SIMILARITY.
                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                            115 AA
                                                                                                                                                                    FRAMEWORK 4
                                                                                                           FRAMEWORK
                                                                                                                               FRAMEWORK
                                                                         InterPro: IPR003006; -. Pfam; PF00047; 1g; 1. Immunoglobulin V region; Bence-Jones
Clin. Invest. 52:1276-1281(1973)
                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=70063440; Pubmed=4188189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-68242259; PubMed-5586923;
                                                                                                                                                                                              12316 MW;
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                                                                                                                                                                                                                          60.18;
69.68;
                                                                                                                                                                                                                                  Local Similarity 69.69 for the 18 Conservative
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102
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                                                                 PIR; A01888; K2HUTW.
                                                                                                                                                                                             113 AA;
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62
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103
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21-JUL-1986
                                                         MARKER
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P01614;
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KV2A_HUMAN
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Length 115;

DB 1;

59.9%; Score 416.5;

Query Match

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                      Gaps
                                          DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKS-YGNTYLSWYLHKPGQSPQLLIYGISNR 79
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      ï
                                                                                                                     80 FSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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 72.6%; Pred. No. 7.8e-35;
tive 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCODA39E46DB96BE CRC64;
                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION FR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.10V-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 AAPPA CHAIN V-III REGION HAH PRECURSOR.
HOmo sapiens (Human).
                                                                                                                                                                                                                     113 AA
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Similarity 72.69
82; Conservative
                                                                                                                                                                                                                   STANDARD;
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InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
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Dreyer W.J., Gray W.R., Hood L.E.;

"The genetic, molecular, and cellular basis of antibody formation:
"The genetic, molecular, and cellular basis.";
some facts and a unifying hypothesis.";
cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01887; KZHUML.
                                                                                                                                                                                                                                                                                                                                                                             61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                   1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-III REGION HIC.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                        57.6%; Score 400; DB 1; Length 129; 56.1%; Pred. No. 3.9e-33; ive 28; Mismatches 26; Indels
                                                                                                                                        FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                                              14070 MW; 7395528EA2BB74D6 CRC64;
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65.2%; Pred. No. 9.3e-33;
Live 20; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Bence-Jones protein.
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Bukaryota; Metaron.
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                                                                                                                                                                     JK1 SEGMENT.
BY SIMILARITY.
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                                region; Signal.
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38
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92
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InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region;
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117 WTFGQGTKVEIK 128
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Best Local Similarity
Matches 73; Conserv
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129 AA;
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Best Local Similarity
Matches 74; Conserv
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P01616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Muchantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Inplications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

- ANTONAT INDOIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
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                                                                    Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).

-i- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAUTOANTIEODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      IG KAPPA CHAIN V-III REGION HAH. FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 129;
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COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
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14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%; Score 401; DB 1;
56.8%; Pred. No. 3.1e-33;
ive 27; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CH.IN V-III REGION HIC PRECURSOR.
Eukaryota; Hetazoa; Chordata; Craniata; Verteb
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                                             SEQUENCE FROM N.A.
MEDLINE=88171307; PubMed=3127527;
                                                                                                                                                                                                                                                             region; Signal.
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HSSP; P01783; ZMCP.
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HSSP; P01789; 2MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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Best Local Similarity
Matches 75; Jonserv
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                NCBI_TaxID=9606;
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P18136;
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KV2D_MOUSE

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21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                          81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                         Immunoglobulin V region; Monoclonal antibody; Hybridoma
                                                                                                                                                                                                                                                                       12496 MW; 42C019D10ADA3C91 CRC64;
                                                                                                                                                                                                                                                                                                        Score 394; DB 1;
Pred. No. 1.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 17529.1.
                                                                                                                                                                                                                                                                                                                              14; Mismatches
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67.9%;
                                                                                                                                                                                                                                                                                                               watches 76; Conservative
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                                                                                                                                   InterPro; IPR003006; -. Pfam; PF00047; 19; 1.
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P03976;
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KV2E_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
        DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYXCANLQELPYTFGGGTKLEIK 112
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S6.8%; Score 395; DB 1; Length 112;
Best Local Similarity 67.9%; Pred. No. 1e-32;
Matches 76; Conservative 11; Mismatches 25; Indels
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                                                   SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD5EF5E6D789FBEC CRC64;
                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 251.3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-II REGION 7S34.1.
                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin V region; Monoclonal antibody.
                                                                                                                                  112 AA
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75;
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KV4C_HUMAN
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"Mechanisms of antibody diversity: multiple genes encode structurally related mous: kappa variable regions.";
Proc. Natl. icad. Sci. U.S.A. 75:3913-3917(1978).
                                                                      Gaps
                                                                                         21 DVVVTQTFLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                   Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: .mplications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=1(.090;
                                                                                                                                                                                                                                                                                                                                                                                                                               McKean D.J., Potter M., Hood L.E.;
Mouse immunicaboulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                 Length 113;
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                                                 56.4%; Score 392; DB 1; Length 11 67.0%; Pred. No. 2.1e-32; ive 11; Mismatches 26; Indels
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                      4E93797046F8DB33 CRC64;
                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1986 (Rel. 38, Last annotation update)
16 ARPA CHAIN V-III REGION MOPC 63 PRECURSOR
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   BY SIMILARITY.
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MEDLINE=7823.887; PubMed=98179;
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                      MM;
                      12390
                                                   Query Match 56.4
Best Local Similarity 67.0
Matches 75; Conservative
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InterPro; IPN003006; -.
Pfam; PF0004"; ig; 1.
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  23
113
113 AA;
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Score 387.5; DB 1; Length 131; Pred. No. 7e-32;

55.8%;

Query Match Best Local Simi∴arity

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                                                                                              61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                           60 YQQKPGQPPKLIYLASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDP 119
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1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Detection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                           134 AA.
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Nucleic Acids Res. 13:6531-6544(1985)
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MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
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60
75
82
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Matches 76; Conserv
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REVISION TO 76.
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                                              60 WYLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQ 119
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING 3.
JK1 SEGMENT.
BY SIMILARITY.
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14070 MW; CC8957F0FE3B9012 CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
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FRAMEWORK 1
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Pfam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
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121 PWTFGQGTKVEIK 133
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|16 YTFGQGTKLEIK 127
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GenCore version 4.5
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April 13, 2001, 15:39:52 : Search time 56.51 Seconds (without alignments) 273.782 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table:

374700 seqs, 117207915 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

374700 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL_15:* Database :

sp_fung1:*
sp_humen:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:* sp_rodent:* sp_unclassified:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_virus:*

SUMMARIES

091182 mus musculu Q9ul80 homo sapien Q9ul78 homo sapien Q9ul77 homo sapien Q9ul77 homo sapien Q9ul86 homo sapien Q91174 mus musculu Q9ul89 homo sapien Q91185 homo sapien Q91185 homo sapien Q91186 homo sapien Q91187 mus musculu Q9ul83 homo sapien Q91187 mus musculu Q9ul83 homo sapien Q91187 mus musculu Q91176 mus musculu Q910055 oryctolagus Description 0951182 0961180 0961171 096177 096170 0951174 0961179 0971185 0971185 0961183 0961183 0961183 0961183 0971180 0961181 0991181 Query Match Length DB Score 447 412.5 334.5 326.5 326.5 326.5 319.5 319.5 319.5 319.5 311.5 311.5 311.5 311.5 311.5 311.5 311.5 311.5 311.5 311.5 313.5 31

homo homo homo mus mus	O99474 mus musculu O99456 homo sapien O99455 homo sapien O61243 mus musculu P79336 felis silve P77710 rattus norv O94176 homo sapien O94173 homo sapien	Oydwis rattus norvogewis rattus norvogewis rattus norvogewis and salmirt sci Oysmn sanimirt sci Oysmn sanimirt sci Oysmn sanimirt sci Oyyvo homo sapien Oyyvo homo sapien Oyyvo homo sapien Oyib02 sphoeroides Owers cooptithe Oyib05 sphoeroides Oversia son taurus
Q9NSD6 Q9NP29 Q9ULB2 Q9QX57 P97797	09WTN4 09UQ56 09UQ55 061243 061243 PP79336 P97710 09UL76 09UL76	090M15 090L89 090X8M7 091X8M6 095776 091X8M6 091B02 091B05 091B05
7 4 4 4 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		6 113
107 130 107 509 513	100 100 100 100 100 100 100 100 100 100	200 200 200 200 233 337 337 506 506
32.7 30.1 29.7 21.3 21.3 21.0	19.7 109.7 109.7 109.7 10.8 10.8 10.8 10.8	166.6 166.6
227 209.5 206.5 148 148 146	137 132.5 132.5 126.5 125.5 119.5 118.5	115.5 114 110.5 110.5 100.7 107 107 104.5 104.5
20 22 23 24 25		3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

ALIGNMENTS

114 AA.

PRT;

PRELIMINARY;

RESULT 2 Q9UL80 ID Q9UL80 AC Q9UL80;

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81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                              Homo sapiens (Human)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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CN 8.
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SEQUENCE
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                                                                                                                                09UL77
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090YF0
                                                                                               RESULT
Q9UL77
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).

Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9f 06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 SGVPDRF3GSGSGTDFTLKISTIKPEDLGMYYCLQGTH-QPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.2%; Score 356; DB 4; Length 109; 58.9%; Pred. No. 7.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu E., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                 Wu X., Liu B , Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                  12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   59.4%; Score 412.5; DB 4;
69.9%; Pred. No. 1.5e-34;
ive 15; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immuncl. Immunopathol. 87:184-192(1998).
EMBL. AF035(36; AAD56272.1; --
HSSP, P01785; IMCP.
INTERPRO; IF8003006; --
                                                                                                                                                                                                                                                 Clin. Immuno... Immunopathol. 87:184-192(1998).
EMBL; AF0350:4; AAD56270.1; -.
INTERPRO; IPH003006; -.
PFAM; PF0004"; 19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=98277139; PubMed=9614934;
                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE=9827;139; PubMed=9614934;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Simi.arity 69.99
Les 79; Conservative
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NON_TER 109 109
SEQUENCE 109 AA; 116
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Best Local Sim.larity
Matohes 66; Conserv
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RESULT

AC DDT DDT DDT DDT RRY RRY RRY RRY RRY RRY RRY DDR RRT DDR FFT SQ

á qq

Best Loc Matches

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STRAIN=BALB/C; TISSUB-SPLEEN;
shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
method.";
                                                                                                                                                                                                                                                    01-MAY-2000 (TIEMBLEEL 13, Last sequence update)
01-0CT-2000 (TIEMBLEEL 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 48.1%; Score 334.5; DB 4; Length 108; I Similarity 57.1%; Pred. No. 1.1e-26; 64; Conservative 19; Mismatches 24; Indels 5
57 TGIPDRESGSGSTDFTLTISRLEPEDCAVYCQQVGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohart N. Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035037; AAD56273.1; -.
HSSP, P01607; IREI.
INTERPRO; IPR003006; -.
PFAM, PF00047, ig; 1.
                                                                                                                                                                             108 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
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SOR DR SO

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Eutheria; Primates; Catarrhini; Hominidae; Homo
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PFAM; PF00047; 19; 1.
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                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                    63;
          Mammalia;
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NON_TER
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Best Local S
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Q9JL74
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09UL70

09UL70:

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE RECION (FRAGMENT).

Homo sapiens (Human).
                                                                                                                                                                                          Gaps
                                                                                                                                                                          19 GGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
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Έ
                                                                                                                                                                                                                                  79 RFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                  47.0%; Score 326.5; DB 11; Length 298; 53.5%; Pred. No. 2.5e-25; Live 19; Mismatches 29; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
WW X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 326; DB 4; Length 109;
11arity 54.5%; Pred. No. 8.3e-26;
Conservative 25; Mismatches 22; Indels
    EMBL/GenBank/DDBJ databases.
                                         INTERPRO; IPR003006; -
PFAM; PF00047; 1g; 2.
SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD58028; AAD56264.1; -.
INTERPRO; IPR003006; -.
PEAM; PF00047; 19; 1.
                                                                                                                                                                                                                                                                                                                                           109 AA.
                                                                                                                                                                                                                                                                                                                                           PRT;
Gubmitted (DEC-1999) to the
EMBL; AB036341; BAA88633.1;
HSSP; P01607; 1REI.
                                                                                                                 Query Match
Best Local Similarity 53.5%
Matches 61; Conservative
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Local S....
61;
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SEQUENCE
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09UL86;
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Q9UL86
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Q9UL70
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STRAIN-BALB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Wcharacterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206032; AAF69330.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 LPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRFSGVPDRFSGS
                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ů
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

46.0%; Score 319.5; DB 11; Length
Best Local Similarity 59.8%; Pred. No. 3.4e-25;
Matches 61; Conservative 17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 AA; 10939 MW; 3B25D0E784533324 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 GSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                     46.5%; Score 323.5; DB 4;
56.2%; Pred. No. 1.5e-25;
tive 17; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
HSSP; P01607; IREI.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;

"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF206026; AAF69124.1; -

NON_TER 1

NON_TER 103

SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64:
                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bestaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQ-GTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.3%; Score 315; DB 4; Length 109; 53.1%; Pred. No. 1.1e-24; Live 26; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035029; AAD56265.1; -.
HSSP; PO1607; IREI.
PITERPRO: IPR003006; -.
PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel..13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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NON_TER
SEQUENCE
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                                                                                                                                                                              Q9UL85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JL80
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DVVVTQTI'LSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mitazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eucheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                      Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 SGVPDRF: GSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 SGVPSRF:GSGSGTDFTLTISCLQSEDFATYXCQQYXSFPPTFGQGTKVEIK 107
                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

46.0%; Score 319.5; DB 11; Length
Best'Local Similarity 52.7%; Pred. No. 8.6e-25;
Matches 59; Conservative 24; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 46.0%; Score 319.5; DB 4; al Simi]arity 57.1%; Pred. No. 3.8e-25; 64; (Conservative 15; Mismatches 28;
                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF0350:5; AAD56271.1; -.
HSSP; P01607; IREI.
INTERPRO; IFF 003006; -.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                              108
11787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IP3003006; -. PFAM; PF00047; ig; 2.
                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               1(8 AA;
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Best Local Simi]arity
Matches 64; Conserv
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                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                           Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                          Gaps
                                                                                                                                                                    30 SLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRFSGVPDRFSG 89
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).

Busaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                      1;
                                      45.3%; Score 314.5; DB 11; Length 103; 58.3%; Pred. No. 1.1e-24; Live 16; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 44.8%; Score 311.5; DB 4; Length 108; 1 Similarity 51.8%; Pred. No. 2.4e-24; 58; Conservative 27; Mismatches 22; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98277139; Pubmed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                     90 SGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                    fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035031; AAD56267.1; -.
HSSP, P01607; IREI.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                        60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                         Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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Matches 5
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Q9UL83
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schistosoma japonicum (Blood fluke).
Bukaryota, Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
Strigeidida: Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MONOCLONAL ANTI-IDIDOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
"Amplification, cloning and sequence analysis of the light chain
variable region geno of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
HSSP: PO1579: ZFBJ.
INTERPRO: IPRO03006; -.
Young D.C.; ^{\prime} Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 VPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                                                                                       44.6%; Score 310; DB 4; Length 10 llarity 54.5%; Pred. No. 3.4e-24; Conservative 20; Mismatches 25; Indels
                                                                                                                                                                                                                                                               107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 AA; 11478 MW; F20F544426BAE63E CRC64;
                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; P80362; IWTL.
INTERPRO; IPR003006; -.
NOTERRY, PF00047; ig; 1.
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Best Local Similarity
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Peptide
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   RESULT
W53814
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Monoclonal antibod
MAD 1A7 light chai
Light chain variab
Plasmid pGEM-MIL m
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                                                                                                                                                                                           April 13, 2001, 15:35:37 ; Search time 57.59 Seconds (without alignments) 131.022 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                               ....CLQGTHQPYTFGGGTKLEIK 132
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**SIDSI_/gcgdata/geneseqp/AA1980. DAT:**

**SIDSI_/gcgdata/geneseqp/AA1981. DAT:**

**SIDSI_/gcgdata/geneseqp/AA1981. DAT:**

**SIDSI_/gcgdata/geneseqp/AA1983. DAT:**

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**SIDSI_/gcgdata/geneseqp/geneseqp/geneseqp/AA199991.DAT:**

**SIDSI_/gcgdata/geneseqp/genes
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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114.::114.::116.::116.::116.::116.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::120.::12
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                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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559.5
559.5
559.5
554.5
552.5
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Maximum DB &
                                                                                                                                         OM protein
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No.
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VL sequence of ant
Mouse immunoslobul
Chimeric Mah light
BR55-2 light chain
BR55-2 murine IgG3
Humanised murine K
Humanised anti-KC-
Variable region of
IgM chimeric antib
L chain subunit of
Anti-human Fas mon
Anti-human Fas ant
                                                                                                                           Plasmid pGEM Wall wartable light cha R6-5-D6 anti-ICAM-Murine BrE-3 immun Kurine BrE-3 immun Co-1 Light Chain V MAb Co-1 light chain V MAthody against I Wurine antibody IC Murine antibody IC
                                                                                                                                                                                                                                                                   Humanised murine B
Mouse Co-1 light c
Amino acid sequenc
Murine anti-ICAM m
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Murine antibody IC
Murine antibody IC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine Act-1 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "signal peptide"
21..132
R52772
R52790
R70457
Y17416
R32241
                                                                       R70470
W60867
Y80294
W31752
W71889
                                                                                                                  B12909
B23814
W68492
R15199
R11598
R52770
R09424
W06214
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Y00781
W81448
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Y50751
R52806
                                            R31587
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                                                                                                                                                                                                                                                                            W85060
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                                                                                                                                                                                                                                                                                                                                                                           W53814 standard; Protein; 132 AA.
97WO-US13884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0700737
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                Bendig
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g
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                                                                                                                   The present Hequence represents the light chain varaible region of murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Musicosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of th.s particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high andothalial 'emules in mucosal lymph nodes. Humanised Act-1 can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting diseases such as inflammatory bowel diseases. The immunoglobulin can also be used for detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                        61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                     Consensus protein sequence of the murine variable light chain region.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                1 MKLPVRLJVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; Mumanised artibody; murine antigen binding region; inhibition; leukocyte irfiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                            Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graff. versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                          Length 132;
                                                                                                                                                                                                                                                                                                Indels
  Ringler DJ;
                                                                                                                                                                                                                                                                        ; Score 695; DB 19;
; Pred. No. 3e-48;
0; Mismatches 0;
  Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..zu
/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W53817 standard; Protein; 140 AA.
  Newman W,
                                                                                                      Claim 23; Fig 7; 145pp; English
                                                                                                                                                                                                                                                                           Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 132; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                               cones ST,
                                WPI; 1998-15:172/14.
N-PSDB; V200;7.
                                                                                                                                                                                                                                              1 32 AA;
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    Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W53817;
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The present sequence represents the consensus amino acid sequence comprising the variable region of murine Act-1 antibody determined from several independent mouse light chain variable region clones. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadcAw1-) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to madcAw1, which is present of high endothelial venules in mucosal cylmph nodes. Variable regions were amplified from DNA encoding Act-1 using degenerate PCR primers V20083-84. The degeneracy of the PCR primers v20083-84. The degeneracy of the PCR primers consensus sequence. The present sequence was used to construct consensus sequence. The present sequence which contain murine antigen conneric, humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit can be used to inhibit can be used to inhibiting leukcoyte confilteration of tissues, e.g. for treating inflammatory diseases such as inflatmatory bowel disease. The immunoglobulin can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLPVRLLVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTVLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse: Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; Mumanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                      Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light chain of a humanised murine Act-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 695; DB 19;
100.0%; Pred. No. 3.2e-48;
tive 0; Mismatches 0;
                                                                                                                      Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection, isolation and diagnosis.
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                                                                                                                         Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 145pp; English.
96US-0700737
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                                                            (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                     WPI; 1998-159172/14.
N-PSDB; V20086.
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Matches 132; Conserv
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   15-AUG-1996;
                                                                                                                                                               Saldanha J;
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain (W14941) and light chain (W14942) sequences correspond to murine anti-porcine soluble vascular cell adhesion molecule (VCAM) mnoclonal antibody 374 (see also W1493738). They are encoded by a 3F4 human 1gG4 expression plasmid insert (see also T62938). A chimeric antibody specific for porcine VCAM can be produced in transfected host cells. It is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human
                                                                                                                                                                                                                                                                                                                                             Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
            Xenotransplantation; graft rejection; cell interaction; pig;
vascular cell adhesion molecule; VCAM; monoclonal antibody;
chimeric antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenotransplantation; graft rejection; cell interaction; pig;
vascular cell adhesion molecule; VCAM; monoclonal antibody;
chimeric antibody; diagnosis.
                                                                                                                                                                                                                                                              Rollins S;
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80.5%; Score 559.5; DB 18; Length
Best Local Similarity 81.1%; Pred. No. 3e-37;
Matches 107; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                              Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine anti-porcine VCAM 3F4 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 65-66; 105pp; English.
                                                                                                                                                                                                                                                             Matis LA, Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W14937 standard; Protein; 238 AA.
                                                                                                                                                         96WO-US15575
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                                                                                                                                                                                                                             (ALEX-) ALEXION PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA;
                                                                                                                                                                                                                                                                                                                  N-PSDB; T62938
                                                                                              W09711971-A1
                                                                                                                                                       27-SEP-1996;
                                                                                                                                                                                   26-SEP-1996;
28-SEP-1995;
                                                                                                                            03-APR-1997.
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                                                                                                                                                                                                                                                          Evans MJ,
Rother RP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recipients
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                                                                    Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                               Humanised immunoglobulin reactive with alpha-4-beta-7 integrin
                                                                                                                                                                                                                                                                                                                                                                               used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 138;
                                                                                                                                                                                                                                                                                  Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%; Score 608; DB 19;
87.1%; Pred. No. 2.4e-41;
tive 9; Mismatches 8;
                                                                                                                                                                                                                                                                                 Ponath PD,
                                                              /note= "signal peptide"
21..138
                                                                                                    /note= "mature protein"
                                             Location/Qualifiers
                                                                                                                                                                                                                                                                              Jones ST, Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Fig 12; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W14942 standard; Protein; 238 AA.
                                                                                                                                                                                         97WO-US13884
                                                                                                                                                                                                                     96US-0700737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 87.1
Matches 115; Conservative
                                                                                                                                                                                                                                                 (LEUK-) LEUKOSITE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-159172/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AA;
                                                                                                                                                                                                                                                                                                                                      N-PSDB; V20075
 Mus sp.
Homo saplens.
                                                                                                                             WO9806248-A2
                                                                                                                                                                                       06-AUG-1997;
                                                                                                                                                                                                                  15-AUG-1996;
                                                                                                                                                          19-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1997
                                                                                                                                                                                                                                                                            Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                         Peptide
                                                                                    Protein
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(first entry)

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Variable region coding sequence; constant region epitope; hybridoma; antibody detection; antigen/antibody complex; variable heavy chain.
                                                                                                                                                                                                                                                                                                Use of antibody constant region epitope(s) - as control or calibrator reagents in assays for detecting the presence of
                                       Variable kappa chain of antibody from hybridoma 1-706-139.
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 62-63; 109pp; English.
                                                                                                                                                                                                                                                                                                                           antibody in a test sample
                                                                                                                                                                                                                                           Golden AM, Hackett JR,
                                                                                                                                                                                                                                                                  WPI; 1997-393833/36
                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                               N-PSDB; T98835.
                                                                                                                                                                                                23-JAN-1996;
                                                                                                                            W09727486-A1
                                                                                                                                                                        17-JAN-1997;
                    19-MAR-1998
                                                                                                      Mus musculus
                                                                                                                                                   31-JUL-1997
W34518;
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLPVRILVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                               Lugant cutain (www.sto) and neary untain marson sequences in adhesion provided for the murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAD) 3F4. Hybridoma 3F4 was produced by standard techniques using recombinant, soluble porcine VCAM as immunogen. Chimeric antibodies can be produced by cloning AMD 3F4 and 2A2 (see also W14931-32) variable regions into expression plasmid pAPEX-3P modified to contain the human gamma4 constant region in place of the human gamma1 Cl region. Sequences are provided for 3F4 (chimeric) human GL/G4 coNA (W14940), and 3F4 human IgG4 expression plasmid insert product (W14940), and 3F4 human igG4 expression plasmid insert product (W14941-42). The chimeric antibodies are specific for porcine VCAM. They are useful for diagnosing human regelection of porcine cells, tissues and for improving xenotransplantation of porcine cells, tissues and organs
                                                                                                                                                                                                                                                                                                                 Antibodies binding to porcine but not human cell interaction proteins - seful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3e-37;
9; Mismatches 15: Trail
                                                                                                                                                                                                                                                                                                                                                                                         Light chain (W14937) and heavy chain (W14938) sequences are
                                                                                                                                                                                                                                                Rollins S;
                                                                                                                                                                                                                                                 Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                  Page 52-53; 105pp; English.
                           Location/Qualiflers
                                                                                                                                                                                                                                                 Mitis LA, Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.5%;
81.1%;
                                       43..58
/label= CDR1
                                                              74..80
/label= CDR2
                                                                                  113..121
/label= CDR3
                                                                                                                                                                     96WO-US15575
                                                                                                                                                                                           96US-0004489
95US-0004489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.5
Best Local Similarity 81.1
Matches 107; Conservative
                                                                                                                                                                                                                            (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into human recipients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||||| |||||
120 ftfggg::kleik 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YTFGGG:'KLEIK 132
                                                                                                                                                                                                                                                                                     WPI; 1997-212855/19.
N-PSDB; T62934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AA;
                                                                                                                                                                     27-SEP-1996;
                                                                                                                                                                                           26-SEP-1996;
28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                        WO9711971-A1
                                                                                                                                              03-APR-1997
                                                                                                                                                                                                                                                               Rother RP;
                                                                                                                                                                                                                                                   Evans MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                       Region
                                         Region
                                                                Region
        Mus sp
                                Key
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an

Ostrow DH;

Hoff JA,

97WO-US01074. 96US-0589939.

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This sequence represents the variable kappa chain of the antibody of produced by hybridoma 1-706-139, and can be detected using the method of the invention. The method is for detecting the presence of antibody which can be present in a test sample. It comprises contacting a test sample suspected of containing the antibody with an antigen specific for the antibody to allow the formation of antigen/antibody complexes, detecting the presence of the antibody which may be present in the test sample and employing, as a control or calibrator, a reagent which binds to the cantibody constant region epitopes, where the reagent binds to the antigen and is homogeneous with respect to specificity and affinity. The method can be also be used for detecting the presence of antibodies developed can be also be used for detecting the presence of antibodies developed can be also be used for detecting the presence of antibodies developed contains more than one antigen. The method is used particularly for the detection of human antibodies specific for a given antigen, e.g. HIV-1, hepatitis E virus, rubella virus, etc. Use of the reagents circumwent all coff the problems associated with using an immune sera in the manufacture of the problems associated with using an immune sera in the manufacture coff the problems developed and reproducibly generated in virtually unlimited quantities and are also useful for quantitating, and monitoring the integrity of, the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.4%; Score 558.5; DB 18; Length 131; 81.1%; Pred, No. 1.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.4
Best Local Similarity 81.1
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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W34518 ID W34518 standard; Protein; 131 AA.

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The present sequence is that of the murine anti-idiotype monoclonal antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2. As the glycosphingolipid GD2 is expressed at high density by human neuroectodermal tumours, e.g. malignant melanoma, neuroblastoma, glothoma, soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its CDNA can be used in a vaccine to treat or palliate such diseases. They can also be used to reduce the risk of recurrence of a clinically detectable tumour, and detect an anti-GD2 Ab bound to a tumour cell.

MAb 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 Ab (humoraj response) and
                                                                                                                                                                                                                                                       Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7; variable 11ght chain; ganglioside 2; GD2; 14G2a; neuroblastoma; glycosphingollpid; human; neuroectodermal; tumour; glioma; lung; malignant melanoma; soft tises sarcoma; small cell carcinoma; vaccine; treatment; palliate; detection; diagnosis; recombinant production; purification; probe; primer; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.58 "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining region 3"
                                                                                                                                                                                                         Anti-idiotype monoclonal antibody 1A7 variable light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74..80
/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122..131
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "framework region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..112
ote= "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Socation/Qualiflers
                                                W03199 standard; Protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 1; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                  amplification; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US00882
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                                                                                                                                                  26-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113...121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chatterjee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9622373-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1996;
17-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                    W03199;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                     61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Psoriasis; immunological response; anti-idiotype antibody; gluttate; chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis; monoclonal antibody; 1A7.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                             1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                  The CDNA can be used in expression systems for IA7 prodn., and in the prepn. of probes and primers to respectively assay for IA7
                                                                                      the prepn. of probes and primers to respectively assay for IA7 CDNA, and amplify desired polynucleotides for use in gene therapy
GD2-specific cells (cellular response). It can be used to purify anti-1A7 (Ab3), anti-6D2 (Ab1') or 14G2a (Ab1), detect anti-1A7 on anti-6D2 in a sample or measure the level of cellular anti-1A7 or anti-6D2 activity.
                                                                                                                                                                                                                                 ä
                                                                                                                                                                                            DB 17; Length 149;
                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody 1A7 light chain variable region.
                                                                                                                                                                                           79.8%; Score 554.5; DB 1
79.5%; Pred. No. 4.6e-37;
.ive 10; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y21545 standard; Protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KENT ) UNIV KENTUCKY RES FOUND.
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97US-0065774.
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                                                                                                                                                                                                         Best Local Similarity 79.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chatterjee M, Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                    121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-347407/29.
                                                                                                                                       149 AA;
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                                                                                                                                           Sequence
                                                                                                                                                                                           Query Match
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61 YLHKPGGSPQLLIYGISNRRSGVPDRRSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                Light chain variable region; antibody 1A7; T cell response; melanoma; ganglioside GD2; CDR; complementarity determining region; carcinoma.
                                                          1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20..149
/label= "mature peptide"
/note= "light chain variable region of Ab 1A7"
    Length 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity Determining Region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                Indels
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    Score 552.5; DB 20;
Pred. No. 6.6e-37;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.007
74.007
7.1abel "CDR 2"
7.007
7.007
7.007
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/label= "Framework 4"
132.149
/label= "Constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complementarity
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                                                                                                                                                                                                                                                                                                                                                               Light chain variable region of MAb 1A7
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/label= "Framework 1"
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/label= "Framework
                                                                                                                                                                                                                                                                             Y28468 standard; Protein; 149 AA.
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/label= "CDR 1"
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/label= "CDR 3"
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95US-0372676.
96US-0591196.
     79.5%;
ilarity 79.5%;
Conservative
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                                                                                                                                                                                             121 YTFGGGTKLEIK 132
                      Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1995;
16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1996;
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        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                           Y28468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a monoclonal antibody (MAb) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 - associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the light chain variable region of MAb 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection and treatment of cancers
                                                                                                                                                                               61 YLHKPGQ(:PQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                              Gaps
                                                                                                                       1 MKLPVRLIVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                         Monoclonal autibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastomu; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen.
                                                                                               1;
                                                                   Length 149;
                                                                                               Indels
                                                                                               16;
                                                                    DB 20;
chain variable region of monoclonal antibody 1A7
                                                                 ; Score 554.5; DB 2; Pred. No. 4.6e-37; 10; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chatterjee M;
                                                                                                                                                                                                                                                                                                                                                                                                                               MAb 1A7 ligh: chain variable region.
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                                                                                                                                                                                                                                                                                                                                            Y49209 standard; Protein; 149
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                                                                      79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0591196.
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                                                                                                (onservative
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120 wtfgggtl:leik 131
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N-PSDB; Z31355.
                                                                      Query Match
Best Local Similarity
Matches 105; (onserv
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                            149 AA;
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WO9411508-A.
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                                                                            This polypeptide is the variable light chain region of monoclonal anti-idiotype antibody 1A7. The polypeptide has three CDRs (complementarity determining regions) and four frame work regions. When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The heavy chain variable region of the 1A7 mantibody (Y28469) is also capable of eliciting an anti GD2 response in mammals. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T call and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma (including small cell lung cancer).
                                                                                                                                                                                                                                                                                                                          61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                      1 MKLPVRLLVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                               Single stranded Fv antibody fragment inducing apoptosis in nucleated
                            Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pGEM-M1L mouse MABL-1 L chain V region protein SEQ ID NO:5.
                                                                                                                                                                                                                                             Score 552.5; DB 20; Length 149;
Pred. No. 6.6e-37;
9; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; MABL; IAP; integrin associated protein; single stranded Fv; apoptosis; blood disease; leukaemia; cytostatic.
                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       B23812 standard; Protein; 131 AA.
                                                          Claim 1; Fig 1; 84pp; English.
                                                                                                                                                                                                                                             79.58;
79.58;
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                                                                                                                                                                                                                                                                Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                              121 YTFGGGTKLEIK 132
WPI; 1999-457600/38.
N-PSDB; X89552.
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Best Local Similarity
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The present invention describes a polypeptide containing the variable region of the light chain of a monoclonal antibody, which induces apoptosis, in nucleated blood cells having integrin associate protein (IAP). Also described are: (1) DNA encoding the novel polypeptide; (2) animal or microbial cells expressing the DNA of (1); and (3) agents for the treatment of blood disorders which contain the polypeptide. The polypeptide can be used in the treatment of blood disorders such as leukaemia. The present sequence represents the plasmid pGRM-NIL mouse MABL-11, chain V region which is given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; human breast carcinoma; murine anti-human carcinoma monoclonal antibody KC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine KC-4 immunoglobulin light chain variable region (deduced).
cells having integrin associated protein for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 131;
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/note- "putative glycosylation site"
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/label= KC-4_mature_VL-chain
                                                             Claim 4; Page 50-51; 73pp; Japanese.
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/label= CDR3
122..131
/label= FR4
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/label= CDR1
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74..80
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Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                present invention.
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                     leukemia
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/label= CDR1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                    (CANC-) CANCER
                                                                                                      Modified-site
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08-OCT-1993;
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R70457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YLHKPGQ SPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLPVRL:VLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin variable domain; primer; polymerase chain reaction; chimeric antibody; human milk fat globule; human breast carcinoma; murine anti-human carcinoma monoclonal antibody KC-4.
                                                                                                                                                                                                                                                                                              An initial isolation of cDNAs coding for murine anti-human breast carcinome and) KC-4 was performed using PCR with commercially available pr.mers (see 66751-062758, available from NOVAGEN). Subsequent c.oning using PCR primers JO20, JO21, JO22 and JO24 (see 662759-162762) resulted in the isolation of the mouse Ig variable domuins. The amplified cDNAs were sequenced (062763 and 062764) and immino acid sequences were deduced from them. Chimeric mouse-human intibodies were constructed using human constant regions so as to produce less immunogenic polypeptides which retained the anti-human carcinoma binding specificity of KC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine KC-4 immunoglobulin light chain variable region (deduced).
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                                                                                                                                                                                                         Chimeric human-murine polypeptide(s) specific for human mammary fat globule antigen - for imaging, diagnosing and treating neoplasia, with less undesirable immunogenic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.9%; Score 548.5; DB 15; Length Best Local Simi.arity 78.8%; Pred. No. 1.2e-36; Matches 104; Conservative 10; Mismatches 17; Indels
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/label= KC-4_mature_VL-chain
                                                                                                                                       (CANC-) CANCIIR RES FUND CONTRA COSTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R52790 standird; Protein; 131 AA.
                                                                            92US-0977706.
92US-0977707.
93US-0128015.
                                               93WO-US11316.
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/label= F
43..58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 11 AA;
                                                                                                                                                                                  N-PSDB; Q62763.
                                                                            13-NOV-1992;
13-NOV-1992;
28-SEP-1993;
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                                                15-NOV-1993;
                   26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An initial isolation of cDNAs coding for murine anti-human breast carcinoma MAb KC-4 was performed using PCR with commercially available primers (see Q62776-Q62783, available from NOVAGEN). Subsequent cloning using PCR primers JO20, JO21, JO22 and JO24 (see Q62784-Q62787) resulted in the isolation of the mouse Ig variable domains. The amplified cDNAs were sequenced (Q62788 and Q62789) and amino acid sequences were deduced from them. Chimeric mouse-human antibodies were constructed using human constant regions so as to produce less immunogenic polypeptides which retained the anti-human carcinoma binding specificity of KC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New analogue peptide(s) comprising antibody variable regions used to develop prods. for use in the detection, diagnosis, therapy and prevention of neoplasms
                                                                                                                                                                                "putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceriani RL, Do Couto FJR, Padlan EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES FUND CONTRA COSTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 26; Page 61; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R70457 standard; Peptide; 131 AA.
                                                                                                                                                                                putat
113..121
/label= CDR3
122..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0977696.
93US-0129930.
93US-0134346.
59..73
/label= FR2
74..80
                                                    74..80
/label= CDR2
                                                                                                                                                                                                                                                  122..131
/label= FR4
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98..100
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                                                                                                                                                                                                                                                                                                              were prepared by PCK from Dolyadenylated RNA isolated from 100 million KC-4 hybridoma cells. All clones were obtd. from independent PCRs. The sequences of the primers are given in Q87519-Q8756. The sequences of the primers are given in Q87519-Q8756. In the PCR products were cloned, without prior purificn., into pCR1000 (Invitrogen) and sequenced in both directions. The VL DNA sequence and tis derived protein sequences are shown in Q87531 and R70449-R70457. The mature VL chain begins at AA D of framework i (FRI). VL is a group II kappa chain. Part of the CDR3 and all of the FR4 are encoded by JK2. There is a an asparagine glycosylation site in the sequence of R70449-R70456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLPVRLLVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οŧ
                                                                                                                                                                                                                                                                                                       cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL
                                                                                                                                                                                                                                        New humanised anti-KC-4 monoclonal antibody - used for detection cancer cells, in vivo imaging, ex-vivo purging and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 548.5; DB 16; Length 131; Pred. No. 1.2e-36;
                                       Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
                   VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                 (CANC-) CANCER RESEARCH FUND CONTRA COSTA,
                                                                                                                                                                                                                                                                                 Example; Table 14, Page 31; 61pp; English.
                                                                                                                                                                                        Peterson JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse immunoglobulin E light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y17416 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%;
78.8%;
                                                                                                                            93WO-US11444.
                                                                                                                                              93US-0134346
 (first entry)
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                                                                                                                                                                                      Ceriani RL, Docouto JJR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.89
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AA;
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27-0CT-1995
                                                                                                                         16-NOV-1993;
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                                                                                                    20-APR-1995
                                                             Synthetic.
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The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is substances i.e. with antiallergic activity, to affect any aliesgic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present can mouse immunoglobulin E (IgE) light chain, given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.6%; Score 546.5; DB 20; Length 78.0%; Pred. No. 3.2e-36; Live 11; Mismatches 17; Indels
                                                                                                   Yonemawa
                                                                                                                                                                                                                                                                                                                                         (SANY ) SANKYO CO LTD.
(TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic non-human animal allergy models
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Job time: 118 sec
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                                          Location/Qualifiers
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                                                          /label- signal
20..238
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                                                                                                                                                                                                                                                        13-NOV-1998;
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                                                                                                                                                                  EP921189-A1.
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Peptide
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April 13, 2001, 17:37:55; Search time 4.45 Seconds (without alignments) 51.491 Million cell updates/sec
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Sequence 16, Ap
Sequence 17, Ap
Sequence 17, Ap
Sequence 11, Ap
Sequence 20, Ap
Sequence 20, Ap
Sequence 20, Ap
Sequence 20, Ap
Sequence 22, Ap
Sequence 5, Ap
Sequence 6, Ap
Sequence 6, Ap
Sequence 6, Ap
Sequence 17, Ip
Sequence 17, Ip
Sequence 61, Ap
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06.NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08.NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08.NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-739-449-11472
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US-09-509-031-4

US-09-509-031-11

US-09-509-031-15

US-09-509-031-6

US-09-108-11-6

US-09-108-11-6

US-09-108-11-16

US-09-11-108-2

US-09-11-108-2

US-09-11-108-2

US-09-11-108-2

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US-09-11-108-1

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                                                                                                                                                                                                                                                   7695 segs, 1735856 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length DB
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	~	US/09782504 Tom, Ingegerd Tom, Karl Erlk Kum Folger Lu, Clay Ew, Stephen N: ANTIBODIES ES: 4 DRESS: GRECINOMAS ES: 4 DRESS: GRECINOMAS ES: 4 DRESS: FIFTH Avenue, See Ingeron RICOMA ROCOMPALIBLE FORM: FORM: FORM: FORM: ROSPY TOMINGBER: ROSPY TOMINGBER: ROSPY TOMINGBER: TOMINGBE	; Score ; Pred. 10; Mis
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		L IV. PPLJ PPLJ PPLJ PPLJ PPLJ PPLJ PPLJ PPL	Match Ocal Sim s 84;
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Query Match
Best Local Similarity
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US-09-509-031-6
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APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILLE REPERENCE: 134.74
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILINC DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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US-09-509-031-16
                      1; Gaps
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SGG----IVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLI 73
                                                                          74 YGISNRFYGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
                                                                                              APPLICANT: Suiss, dabriele M.
APPLICANT: Ta::linton, David M.
APPLICANT: Ta::linton, David M.
APPLICANT: Ta::linton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING STITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.7%; Score 366.5; DB 5 Best Local Similarity 62.6%; Pred. No. 7.4e-31; Matches 72; Conservative 16; Mismatches 26
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                                                                                                                                                                                                              Sequence 4, Application US/09509031
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Art [ficial Sequence
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APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
                                                                                                                                                                                                                                                                                                                                                                    A METHOD OF PRODUCING SAME
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DVVVTQTPLSLPVSFGDQVSISCRSSQS-LAKSYGNTYLSWYLHKPGQSPQLLIYGISNR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGN--TYLSWYLHKPGQSPQLLIYGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: TLHL protein
                                                                                   SNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYXCQQXXSTPXSFGQGTKLEIK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Kappa OTHER INFORMATION: protein sequence US-09-509-031-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 7.8e-30;
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Pred, No. 3.1e-30;
                                                                                                                                                                                                                                                                                                APPLICANT: Suess, Cabriele M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A M.
FILE REPRENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT PILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
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CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                       ; Sequence 11, Application US/09509031
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09509031
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
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milarity 61.9%; 1
Conservative 16;
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61.9%;
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APPLICANT: Suess, Gabriel
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Matches 70; Conserv
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US-09-509-031-6
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APPLICANT: Hanna, Nabli A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reft Mitchell E.
APPLICANTION: THEREBELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: LYMPHONA
TITLE OF INVENTION: LYMPHONA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
           55 HWFQQKPGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                                              Sequence 4, Application US/09386658
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575-54182/JPW/SHS/MWM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.7%; Score 303.5; DB 5;
52.7%; Pred. No. 3e-25;
11ve 19; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08475815A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Darrell R. APPLICANT: Hanna, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06
FILING DATE: 07-JUN-1995
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                                                     119 OPYTFGGGTKLEIK 132
                                                                               115 NPPTFGGGTKLEIK 128
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Best Local Similarity
Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: mouse
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US-08-475-815A-11
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APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: BADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
TITLE OF SEQUENCES: 11
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      Gaps
                                   21 DVVVTQTPLSLPVSFGDQVSISCRSSQS-LAKSYGNTYLSWYLHKPGQSPQLLIYGISNR 79
                                                              59 SWYLHKPGOSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTH 118
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                                                                                                                                               Length 128;
    26; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
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1100 New York Avenue, N.W., Ninth FL.
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Pred. No. 3.3e-25;
; Mismatches 40
  16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FLING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 7, Application US/08475815A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Darrell R.
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Best Local Similarity 47.8%; Promatches 64; Conservative 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 235
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
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amino acid
Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 0 CLASSIFICATION:
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APPLICANT:
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US-08-475-815A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                     60 PGRGLEY IGAIYPGNGDTSYNQKFKGKATLTADKSSSTAY-MQLSSLTSEDSAVYYCARS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LLFWIP/SGG---DVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VLLLFW1PVSGGDVVVTQTPLSLP----VSFGDQVSISCRSSQSLAKSYGNTYLSWYLHK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 132;
                                                                                                                                                                                                                                                                                  14.5%; Score 101; DB 4; Length 140; 26.4%; Pred. No. 0.00014; tive 26; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Elianger. Bernard
APPLICANT: Clen, B1-Xing
TITLE OF INVERTION: ANTHEODIES SPECIFIC FOR FULLERENES
FILE REFERENCI:: 0575-54182/JPW/SHS/NVM
CURRENT FILIN: DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 90.5; DB 5;
; Pred. No. 0.0015;
31; Mismatches 49;
                                                                             23522-0157
US 07/978,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-386-658-2; Sequence 2, Application US/09386658; GENERAL INFORM/11ON:
                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 2352
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
                                                         35,030
                                                                                                                                            INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.0%;
Best Local Sim.larity 25.0%;
Matches 33; Conservative 31
               FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            : 140 amino acids
amino acid
                                                                                                                                                                                                                                                                                                         Best Local Similarity 26.4
Matches 34; Conservative
                                                                                                                                                                                                                          , MOLECULE TYFE: protein US-08-475-815A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ); ORGANISM: mouse [murine] US-09-386-658-2

√ 120 AY-WGQ 3TLLTV 130

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LENGTH: 132
                                                                                                                                                                               LENGTH:
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RESULT 10: US-09-533-077-331

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APPLICANT: Fong, Sherman
APPLICANT: Audrey Goddard
APPLICANT: Audrey, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE TITLE OF INVENTION: COMPOSITIONS FILE REPERENCE: P1624R2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 TYLSWYLHKPGQSPQLLIYGISNR----FSGVPDRFSGSGSGTDFTLKISTIKPEDLGMY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 ---KWKYEKPDGSPVFIAFRSSTKKSVQYDDVPEYKDRLNLSENYTLSISNARISDEKRF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 VVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRFSG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 RLLVLLLF------WIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltenya S.
APPLICANT: Bangur, Chaltenya S.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C5
CURRENT APPLICATION NUMBER: US/09/533,077
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 800
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 334
LENGTH: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%; Score 74; DB 5; Length 582; 22.0%; Pred. No. 0.42;
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Sequence 334, Application US/09533077 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 12, Application US/09808689; GENERAL INFORMATION:
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Best Local Similarity 22.09
Matches 27; Conservative
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; ORGANISM: Homo sapiens
US-09-808-689-12
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sharis, Christiaan M.
APPLICANT: Sharis, Christiaan M.
APPLICANT: Sharon, Mu X.
APPLICANT: Bone, Thomas Charles
APPLICANT: Covey, Todd
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 99-513-A
CURRENT APPLICATION NUMBER: US/09/815,108
CURRENT FILING DATE: 2001-03-22
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID MOS: 22
NUMBER OF SEQ ID MOS: 22
SOFTWARE: PATCHIN Ver. 2.0
                                                                      223 VLTGTHPVNTTVDFGGTTSFQCK----VRSDVKPVIQWL-----KRVEYGSEGRHN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                       23 VVTQT-PLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRFS 81
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Pred. No. 0.64;
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                Sequence 20, Application US/09815108
GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
APPLICANT: Sharon, Mu X.
                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 24.3%;
Matches 28; Conservative 10
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Best Local Similarity 24.3%
Matches 28; Conservative
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; LOCATION: (355)..(375)
US-09-815-108-3
US-09-815-108-20
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Gaps

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APPLICANT: Ala, Min
APPLICANT: Ala, Min
APPLICANT: Booker, Thomas Charles
APPLICANT: Covey, Thomas Charles
APPLICANT: Covey, Thomas Charles
TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
TITLE OF INVENTION: USES Thereof
FILE REFERENCE: 99-513-A
CURRENT APPLICATION NUMBER: US/09/815,108
RIOR APPLICATION NUMBER: 60/191,379
PRIOR FILING DATE: 2000-03-22
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GENERAL INFORMATION:
APPLICANT: Saria, Christiaan M.
APPLICANT: Sharon, Mu X.
APPLICANT: Sharon, Mu X.
APPLICANT: Sharon, Thomas Charles
APPLICANT: Boone, Thomas Charles
APPLICANT: Covey, Todd
TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
TITLE OF INVENTION: USBS Thereof
FILE REFERENCE: 99-513-A
CURRENT APPLICATION NUMBER: US/09/815,108
CURRENT APPLICATION NUMBER: 60/191,379
PRIOR FILING DATE: 2000-03-22
MINDERS OF STATES OF THE STATES OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: murine FGFR-L; OTHER INFORMATION: extracellular domain-Fc fusion polypeptide US-09-815-108-22
                                                        270 STIDVGGQKFVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSF 324
82 GVPD----RFSGSGSGTDFT-----LKISTIKPEDLGMYYCLQGTHQPYTF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 STIDVGGQKFVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYLCLGANTMGYSF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 GVPD----RESGSGSGTDFT-----LKISTIKPEDLGMYYCLQGTHQPYTF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 529;
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                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09815108
GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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SOFWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 594
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US-09-815-108-2
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US-09-815-108-22
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LENGTH: 529
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Length 594;

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Score 69.5;

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Query Match

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                    Best Local Simi.arity 24.3%; Pred. No. 1.2;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps
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Search completed: April 13, 2001, 17:37:56 Job time: 172 sec

Sequence 10, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 1, Appl Sequence 11, App

Sequence 11, A Sequence 52, A Sequence 45, A Sequence 45, A Sequence 45, A Sequence 45, A Sequence 18, A Sequence 80, A Sequence 80, A Sequence 60,
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Run on:

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Searched:

Database

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APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ones, S. Tarran
APPLICANT: Jones, S. Tarran
APPLICANT: Saldana, Walter
APPLICANT: Saldana, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
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US-08-700-737-52
US-08-286-754-45
US-08-408-724-45
US-08-472-819-45
US-08-487-113C-45
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US-09-382-289-45
US-09-046-351-78
US-09-046-351-82
US-09-046-351-82
US-08-827-223-82
US-09-046-351-80
US-09-046-351-80
US-09-046-351-80
US-09-046-351-80
US-09-1866-4
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US-09-523-095A-10
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US-08-665-839B-60
US-09-454-925A-10
                                                                                                                                                                                                                                                                                         US-07-977-706C-11
US-07-977-707B-11
US-08-128-015-11
                                                                                                                                                                                                                                                                    US-07-977-706A-11
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US-07-946-314-3
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NAME: BROOK, DBV1d E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08700737 GENERAL INFORMATION:
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STATE: Massachusetts
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1 MKLPVRLLVLLLFWIPVSGG.........CLQGTHQPYTFGGGTKLEIK 132
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Sequence 6, 1
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Sequence 2,
Sequence 2,
Sequence 2,
Sequence 2,
Sequence 6,
Sequence 6,
                                                                                                                                                                                        April 13, 2001, 17:37:47 ; Search time 117.03 Seconds
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/cgn2_6/ptodata///paa/vlS085_COMB.ppp:*
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/cgn2_6/ptodata///paa/vlS093_COMB.ppp:*
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ptodata/2/paa/US095_COMB.pep:
ptodata/2/paa/US096_COMB.pep:
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-700-737-6
US-08-700-737-21
US-08-700-737-7
US-09-324-191-2
US-09-293-533-2
US-09-293-533-2
US-08-134-346A-50
US-08-134-346A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1009251 seqs, 160854530 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Result Š

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TOPOLOGY:
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                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fingler, Douglas J.
APPLICANT: Fingler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Lendig, Walter
APPLICANT: Eendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: MITTERSIN
NUMBER OF SECUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                   Length 132;
                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                 100.0%; Score 695; DB 11;
100.0%; Pred. No. 3.3e-61;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FAREHLIN RELEASE TO CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATI: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGET INFORMATION:
NAME: Brock, David E.
REGISTRATICN NUMBER: 22,592
REFERENCE/IOCKET NUMBER: LKS95-10
TELECOMMUNIC/IION INFORMATION:
TELECOMMUNIC/IION INFORMATION:
TELEFEXX: (617) 861-6240
INFORMATION FO: SEQ ID NO: 6:
SEQUENCE CHAIACTERISTICS:
SEQUENCE CHAIACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYP: Floppy disk
COMPUTER: IBM PC compatible
OPERATING (YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08700737 GENERAL INFORM*TION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 861-6240
TELEPAX: (517) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPPE: amiro acid
TYPPE: amiro acid
OLEGIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPH: protein US-08-700-737-6
                                                                                                                              MOLECULE TYPE: protein US-08-700-737-12
                                                                                                                                                                                                                                                                                                                                                                                                                     121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                    121 YTFGGGTKLEIK 132
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Best Local Similarity
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                                                                                                                   TOPOLOGY:
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                                                                                                                                           Gaps
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                                                                                           1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Porath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldania, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4
TITLE OF INVENTION: 1NTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                    ;
   Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 138;
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                                    Indels
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STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DAP: APPLICATION NUMBER: US/08/700,737 FILING DATE: 15-AUG-1996
Score 695; DB 11;
Pred. No. 3.6e-61;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 616; DB 11;
Pred. No. 2.4e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08700737 GENERAL INFORMATION:
                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORREY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
   100.0%;
illarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.68;
87.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.69
Best Local Similarity 87.99
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-700-737-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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                   Best Local Similarity
Matches 132; Conserv
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; Sequence 2, Application US/09293533 ; GENERAL INFORMATION:
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COGANISM: Mus Musculus
US-09-192-838-2
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US-09-293-533-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
61 YLOKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nones, S. Tarran
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Sandanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.3%; Score 593; DB 11;
100.0%; Pred. No. 3.6e-51;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
REGISTATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 861-6240
TELEFAX: (617) 861-6340
TELEFAX: (617) 861-9540
                                                                                                                                                                Sequence 7, Application US/08700737 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09192838 GENERAL INFORMATION:
                                                                                                                                                                                                   APPLICANT: Ponath, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                         121 YTFGQGTKVEIK 132
                                    121 YTFGGGTKLEIK 132
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US-08-700-737-7
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                                                                                                                                               US-08-700-737-7
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GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: CHATTERIEE, Malaya
APPLICANT: CHATTERIEE, Malaya
APPLICANT: FOON, Kennech A.
TITLE OF INVENTION WETHOOS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REPERENCE: 304142000540
CURRENT APPLICATION NUMBER: US/09/324,191
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: 60/065,774
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
SED ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
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                                                                                                                                                                                                                                                                                                                  79.8%; Score 554.5; DB 79.5%; Pred. No. 3.2e-47 Live 10; Mismatches 10
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Best Local Similarity 79.5%; Pred. No. 3.2e
Matches 105; Conservative 10; Mismatches
CURRENT APPLICATION NUMBER: US/09/192,838
CURRENT FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 60/065,774
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 2
LENGTH: 149
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 79.58
Matches 105; Conservative
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Sequence 50, Application US/08134346A

Sequence 50, Application US/08134346A

GENERAL INFORMATION:
APPLICANT: Gor Couto, F.J.R.
APPLICANT: Ceriani, R.L.C.
APPLICANT: Petersen, J.A.
TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                     61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                                                                                                                                                                                                                                                                                            60 YLQKPGQSPKLLIXKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVP 119
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                                                                                                                                                                                                                                                                               1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                         Score 550.5; DB 19; Length 131;
Pred. No. 7e-47;
3; Mismatches 17; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                          8; Mismatches
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STREET: 300 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Onofrio, Dara L.
REGISTRATION UNBER: 34,889
REFERENCE/DOCKET UNBER: CLT 1
TELECOMMUNICATION INFORMATION:
TELEFAM: 212-826-6565
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            Query Match 79.2%;
Best Local Similarity 80.3%;
Matches 106; Conservative
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SEQ ID NOS: 40 Patentin Ver. 2.1
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Best Local Similarity 77.3
Matches 102; Conservative
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  NUMBER OF SEQ ID NOS:
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                                                                                                          ; ORGANISM: Mus sp.
US-09-523-095A-6
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US-08-134-346A-50
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                                         SEQ ID NO 6
LENGTH: 13
                                                                                        TYPE: PRT
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           APPLICANT: Soon, Kenneth A.
APPLICANT: Soon, Kenneth A.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEDULENCES: 6
CORRESPONDEN: ADDRESS:
ADDRESSES: MORRISON & FOERSTER
STREET: 75 PAGE MILL ROAD
STATE: 6A
CUTY: PAL) ALTO
CUTY: PAL) ALTO
STATE: 6A
COUNTRY: JSA
ZIP: 9430-1018
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APPLICANT: K.KUCHI, YASUGUMI
TITLE OP INVEHTURIN: APOPTOSIS-INDUCING SINGLE-CHAIN FV
FILE REFERENCI: 065678/0102
CURRENT APPLICATION NUMBER: US/09/523,095A
CURRENT FILIN: DATE: 2000-03-10
PRIOR APPLICANION NUMBER: JP 11-63557
PRIOR FILING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                             COMPOURER REAJABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PROG APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
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Sequence 6, Aprilication US/09523095A
GENERAL INFORM.TION:
APPLICANT: FUKUSHINA, Nacshi
APPLICANT: UNIO, Shinsuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
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INFORMATION FCR SEQ ID NO:
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120 WTFGGG/KLEIK 131
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Best Local Similarity
Matches 105; Conserv
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TOPOLOGY:
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                                                                 1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
                                                  61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP
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                                                                                                                                                                                                                 APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Pedian Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          E: Pretty, Schroeder & Poplawski 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P6639938
                                                                                                                                                                            US-08-976-288A-95
; Sequence 95, Application US/08976288A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 131 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-976-288A-95
                                                                                                      121 YTFGGGTKLEIK 132
                                                                                                                   120 YTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                              Los Angeles
California
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STREET: 44'
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                            Gaps
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GENERAL INFORMATION:
APPLICANT: Tsuruo, Takashi
APPLICANT: Hamada, Hirofumi
APPLICANT: Hamada, Hirofumi
APPLICANT: Kurosawa, Yoshikazu
TITLE OF INVENTION: Chimeric Antibody Against Drug-Resistant
TITLE OF INVENTION: Cancers and Process for Production Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 131;
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Camposil & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
COUNTRY: United States
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUW TYPE: FIOPPY disk
COMPUTER: IBM PC COMPATIDLE
OMPUTER: IBM PC COMPATIDLE
OMPRATIOS STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,044
FLING DATE: O'-JUN-1995
CLASSIFICATION NUMBER: 31,815
RECTARATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFEREN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-827-223-10
Sequence 10, Application US/08827223
GENERAL INFORMATION:
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amino acid
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Best Local Similarity 78.0°
Matches 103; Conservative
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Sequence 10, Application US/09523095A; GENERAL INFORMATION:
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APPLICANT: Serizawa, Nobufusa
                                                                                                                                                          77.18;
78.08;
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-046-351-10
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NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver.
SEQ ID NO 10
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                         121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Mus musculus US-08-827-223-10
                                                                                                                                                                           Best Local Similarity
Matches 103; Conserv
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US-09-523-095A-10
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US-09-046-351-10
                                                  LENGTH: 238
TYPE: PRT
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                                                       APPLICANT: Conchara, Shin
TITLE OF INVINITION: ANTI-Fas RECOMBINANT ANTIBODIES AND DNA THEREFOR
NUMBER OF SEQUENCES: 80
CORRESPONDENTE ADDRESS:
ADDRESSEE: Frishauf, Holtz, Goodman, Langer & Chick,
ADDRESSEE: P.C.
STREET: 7.37 Third Avenue
CITY: New York
STATE: New York
COUNTRY: Inited States
ZIP: 1001'-2023
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Sequence 10, Application US/08827223A

Sequence 10, Application US/08827223A

GENERAL INFORMY: Selizawa, Nobufusa

APPLICANT: Selizawa, Kanihisa

APPLICANT: ICLIKawa, Kimihisa

APPLICANT: ICLIKawa, Kimihisa

APPLICANT: ICLIKawa, Shin

TITLE OF INVERTION: ANTI-Fas RECOMBINANT ANTIBODIES AND DNA THEREFOR

FILE REFERENCH: 970093/HG

CURRENT APPLICATION NUMBER: US/08/827,223A

CURRENT FILIN: DATE: 1998-07-23

BEARLIER APPLICATION NUMBER: JP Hei 8-78570

EARLIER FELIN: DATE: 1996-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 535.5; DB 12; Length 238; 78.0%; Pred. No. 4.2e-45;
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APPLICATION DATA: 27-MAR-1997 CLLSSFICATION: 536 CURSEFICATION: 536
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APPLICATION DATA:
APPLICATION NUMBER: JP Hei 8-78570
FILING DATE: OI-APPR-1996
ATTOMICYAGENT INFORMATION:
NAME: GOOJMAN, HETDERT
REGISTRATION NUMBER: 17081
TELECHONE: 212-319-4900
                                       Chikawa, Kimihisa
Conehara, Shin
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INFORMATION FCR SEQ ID NO: 10:
                           Kaori
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amino acid
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Best Local Similarity 78.05
Matches 103; Conservative
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COMPUTER REA JABLE FORM:
MEDIUM TYP3: Floppy of
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                           Nakahara,
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APPLICANT:
APPLICANT:
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                      Gaps
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                                                                                                                            Length 238;
Length 238;
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                                                      18; Indels
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APPLICANT: Takahashi, Tohru
APPLICANT: Nakahasa, Kaori
APPLICANT: Nakahasa, Kaori
APPLICANT: Vonehara, Kaori
APLICANT: Vonehara, Shin
TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
TITLE REFERENCE: 980125/MG
CURRENT APPLICATION NUMBER: US/09/046,351A
CURRENT PELLING DATE: 1998-03-23
EARLIER APPLICATION NUMBER: JP HEI 9-67938
SARLIER APPLICATION NUMBER: JP 7-03-21
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
     DB 12;
     Score 535.5; DB 1; Pred. No. 4.2e-45; 10; Mismatches 18
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APPLICANT: UNO, Shinsuke
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APPLICANT: KIKUCHI, Yasufumi

TITLE De INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV

TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV

CURRENT PAPLICATION NUMBER: 2000-03-10

PRIOR APPLICATION NUMBER: 2000-03-10

PRIOR APPLICATION NUMBER: 300-03-10

PRIOR APPLICATION NUMBER: 300-03-10

PRIOR APPLICATION NUMBER: 300-310

SEQ ID NO. 10

LENGTH: 131

TYPE: PRT

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(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-153-171-5

US-08-053-171-5

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US-08-129-930B-95

PCT-US91-02945-3

PCT-US91-02946-3

US-07-930B-11

US-08-129-930B-11

US-08-129-930B-11

US-08-138-138-45

US-08-483-389-45

US-08-483-389-45

US-08-483-932-45

US-08-483-932-45

US-08-473-503-45

US-08-473-503-45

US-08-473-680-45

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US-08-392-338A-21 US-08-166-093-21 US-09-166-093-21 US-09-166-094-21 US-09-166-094-21 US-09-166-094-21 US-09-166-094-11 US-09-166-093-11 US-09-166-093-11 US-09-166-093-11 US-09-166-093-11 US-09-166-093-15 US-09-166-093-15 US-09-166-093-15 US-09-166-093-15		Score Pred. 9; Mis
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00000000000000000000000000000000000000	Application US/085899 6015662 EPORMATION: TT: Hackett, Jr., John TT: Hoff, Jane A. TT: Golden, Alan M. TT: Golden, David H. TT: Golden, David H. TT: Golden, Alan M. TT: Golden, David M. TT: Golden M. TT: Golde	/ Match Local Similarity hes 107; Conser
831 831 831 831 831 831 831 831 831	1 -939-7 NO. 60156 L. INFORMA I. INFORMA I. INFORMA I. INFORMA I. INFORMA I. INFORMA I. I. INFORMA I. I. INVER E. OF INVER E. OF INVER E. OF INVER E. OF INVER E. OF SEQUENCE I. Abbod I. T.	Simi 7;
 	1 19.939-7 ence 7, Applint No. 601566 Ence 7, Applint No. 601566 Ence 7, Applint No. 601566 Encline No. 601566 Encommunication For Filter No. 601566 Encline No. 6015666 Encline No. 6015666 Encline No. 6015666 Encline No. 6015666 Encline No. 60156666 Encline No. 601566666 Encline No. 6015666666 Encline No. 601566666666666666666666666666666666666	atch cal 10
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RESULT 4
US-09-192-545-4
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                                                                        60 YLQKPGQS PKILIIYKVSNRFSGVPDRFSGSGSGTDFTLKISKVEAEDLGVYFCSQSTHVP 119
                                                                                                                                                                                                                                                                                           GENERAL INFORM.TION:
APPLICANT: (hatterjee, Malaya
APPLICANT: (hotterjee, Sunil K.
APPLICANT: (hotterjee, Sunil K.
APPLICANT: (hotterjee, Sunil K.
APPLICANT: (hotterjee, Sunil K.
TITLE OF INV):NITION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INV):NITION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SE(UDENCES: 66
CORRESPONDENCE ADDRESS:
Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYP: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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Pred. No. 1.5e-46;
9; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGE TY INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/OCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEFRONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER STREET: 7:5 PAGE MILL ROAD CITY: PALO ALTO STATE: CA STATE: CA STATE: USA STATE: USA ZIP: 94301-1018
                                                                                                                                                                                                                                                          Sequence 2, Application US/08752844 Patent No. 5935121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.58;
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LENGTH: 149 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-752-844-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTFGGG1KLEIK 132
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Matches 105; Conserv
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                                                                                                                                                                                                                            RESULT 2
US-08-752-844-2
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Sequent No. 618044

Sequent No. 618044

GENERAL INFORMATION:
APPLICANT: Karasuyama, Hajime
APPLICANT: Taya, Choji
APPLICANT: Matsucka, Kunie
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 799P79570

CURRENT APPLICATION NUMBER: US/09/192,545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08591196
Patent No. 5977316
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Sunil K.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 149;
                                                                                                                                                                                                                                                                                                                                                COMPOURE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOURE: TBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 552.5; DB 2
Pred. No. 1.5e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30414-20002.20
                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION OF A MICHAEL SCHIEF, J. MICHAEL SCHIEF, J. MICHAEL SEGRATION NUMBER: 40,253 REFERENCE/DOCKET NUMBER: 304 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 70614
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
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79.5%;
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Best Local Similarity 79.59
Matches 105; Conservative
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co. Loibner
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSPER: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSITCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-240
TELEFA: (415) 326-242
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acids
TYPE: AMINO acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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120 FTFGSGTKLEIK 131
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US-08-129-930B-95
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                    1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                          Query Match 78.6%; Score 546.5; DB 4; Length 238; Best Local Similarity 78.0%; Pred. No. 1e-45; Matches 103; Conservative 11; Mismatches 17; Indels 1
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                                                                                                                               TYPE: PRT CRGANISM: Artificial Sequence FEATURE: Description of Artificial Sequence: Designed heavy US-09-192-545-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/M-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
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78.2%; Score 543.5; DB 1
Best Local Similarity 78.0%; Pred. No. 9.6e-46;
Matches 103; Conservative 11; Mismatches 17
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: JP HEI 9-313989
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SUPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-053-171-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 LTFGAGTKLELK 131
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROBINSON, MARTYN K
APPLICANT: BRIGHT, SUSAN M
TITLE OF INVENTION: HUMANIZED CHIMERIC ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                       SCHWARE: Patentin Release #1.0, Version #1.25
SCHRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 199104429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Ave. NW Suite 300
STREET: 1225 Connecticut Ave. NW Suite 300
                                                                                                                                                                                                                                                               PRIOR APPLICATION: *35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 833-8716
INFORMATION FOR SEC ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application PC/TUS9102946; GENERAL INFORMATION:
                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROTHLEIN, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 173 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAIR, JOHN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.99
Best Local Similarity 77.39
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein PCT-US91-02942-3
                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                      FILING DATE: 19
CLASSIFICATION:
                                                                               20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US91-02946-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Оp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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PCT-US91-02942-3
PCT-US91-02942-3
Sequence 3, Api-lication PC/TUS9102942
SEQUENCE INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ATHMAL, DILJEET S
TITLE OF INFORMES: 102
NUMBER OF SIQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                      APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
TITLE OF INVINITION: Analogue Peptides With Broad
TITLE OF INVINITION: Analogue Peptides With Broad
TITLE OF INVINITION: Diagnostic Vaccination and
TITLE OF INVINITION: Therapeutic Methods
NUMBER OF SENUENCES: 96
CORRESPONDEN'E ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2155 No. 5804187th Broadway, Suite 201
CITY: Mellut Creek
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTONEY/AGENT TATEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 537.5; DB 1
Pred. No. 3.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                 APPLICANT: (deriani Dr., Fernando J.R. APPLICANT: (teriani Dr., Roberto L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASALFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERCE/DOCKET-NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
        Sequence 95, Application US/08129930B Patent No. 5804.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: n.a.
INFORMATION FCR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.3%;
nilarity 77.3%;
Conservative 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYFE: peptide US-08-129-930B-95
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 YTFGGG:KLEIK 131
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Best Local Similarity
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 94595
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MOLECULE TYPE: peptide US-08-129-930B-11
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US-08-129-930B-11
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Patent No. 5792852

GENERAL INFORMATION:
APPLICANT: Cerland Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
ANDIES OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: Analogue Petides with Specificity
TITLE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLPVRLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
                      FILING DATE: 19910429
CLASSIFTCATION: 435
ATTORNEY/ACTATION: 435
ATTORNEY/ACTATION: 435
ATTORNEY/ACTATION: 435
REGISTRATION NUMBER: 30,353
REGISTRATION NUMBER: 1011.0576600
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 466-0800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
           PCT/US91/02946
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NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 173 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (510) 748-6688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
PCT-US91-02946-3
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YTFGGGTKLEIK 132
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                               Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence II. Application US/08129930B
Fatent No. 5804187
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ceriani Dr., Fernando J.R.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Gaurdo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: AMZEL Ph.D., VIVIANA
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                        Ouery Match 74.7%; Score 519.5; DB 1; Best Local Similarity 77.3%; Pred. No. 2e-43; Matches 102; Conservative 10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: n.a.
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 131 amino acids
amino acid
                                                                                                           MOLECULE TYPE: peptide US-07-977-696C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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RLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKP 65
                                                                                                                                                                                                                                                5;
                                                                                 Length 127;
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STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                              17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389 FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
                                                                          Score 513; DB 1;
Pred. No. 8.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45. Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
CORRESPONDENCE MATCHAIL O'TOOLE, GETSTEIN, M.
                                                                                                                                                 9; Mismatches
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REPERENCE/POCKET NUMBER: 27866/32760
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 05-MAY-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1993
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STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    73.8%;
78.1%;
                                                                                                                                                     Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GGTKLEIK 127
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                                                                                 Query Match
Best Local Simi
Matches 100;
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US-08-483-389-45
US-08-482-882-45
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                                                                                                                                                                                                                                                                                            60 FLQKSGQ:PKLLIYRASIRFSGVPDRFSGSGSETDFTLKISRVEAEDLGVYFCFQGTHVP 119
                                                                                                                                                                                                                                                          61 YLHKPGQS:PQLLIYGISNRFSGVPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQP 120
                                                                                                                             1 MKLPVRLIVLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSW 60
                                                                                                                                                                         Gaps
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   Length 131;
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                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/08482882
Sequence 45, Application US/08482882
Patent No. 5773:18
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: 'Vazeux, Rosemay
TITLE OF INV:NRTION: ICAM-Related Materials and Methods
NUMBER OF SEPJUENCE: 116
CORRESPONDEN:E ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYP:: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATA: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 0 DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE:
ADDITON: A 35
PRIOR DATE:
   Query Match 74.7%; Score 519.5; DB 1; Best Local Similarity 77.3%; Pred. No. 2e-43; Matches 102; Conservative 10; Mismatches 19;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 2:-3856
INFORMATION F(R SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 127 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                     121 YTFGGGTULEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                          60603
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60 GQSPQLLIXKVSNRFSGVPDRFGSGSGSGTDFTLKLSRVEAEDLGVYFCSQSTHVPYTFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GQSPQLLIYGISNRFSGVPDRF-SGSGSGTDFTLKISTIKPEDLGMYYCLQGTHQPYTFG 124
                                                                                                                                                                                                                                                                                                                                                                    6 RLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKP 65
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US-08473-503-45
Sequence 45, Application US/08473503
Fatent No. 5869262
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATIGE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 25-JAN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-JAN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-JAN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 37-JAN-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 37-JAN-1992
APPLICATION NUMBER: 32178
FILING DATE: 37-JAN-1993
ATPORNEY PROPERVATION:
NAME: NO. 5869262and, Greta E.
RESERRATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                      Score 513; DB 2;
Pred. No. 8.3e-43;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerstein, S. Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                Query Match 73.8%;
Best Local Similarity 78.1%;
Matches 100; Conservative
                     SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-113D-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 GGTKLEIK 132
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|120 GGTKLEIK 127
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                                                                                                                                                                                                                                                                                                                66 GOSPQLLIYGISNRFSGVPDRF-SGSGSGTDFTLKISTIKPEDLGMYXCLQGTHQPYTFG 124
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                           6 RLLVLLLFWIPVSGGDVVVTQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chlcago
STATE: 1111nois
STATE: 1111nois
STATE: 1111nois
STATE: 1111nois
COUNTRY: United States of America
LTF: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,113D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-487-113D-45
; Sequence 45, Application US/08487113D
; Patent No. 5837822
; Patent No. 5837822
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TTLLE OF INVENTION: ICAM-Related Materials and Methods
; WUMBER OF SEQUENCE: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
marger: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                Score 513; DB 2; Length 127;
Pred. No. 8.3e-43;
9; Mismatches 17; Indels
                                                                                                                                                                       17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILLING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,754

FILING DATE: 05-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/102,852

FILING DATE: 25-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266

FILING DATE: 25-AUR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-UN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/899,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/897,689

FILING DATE: 27-AN-1992

ATTORNEY/AGENT INFORMATION:

ANDELS AND SA37872AND GATER FELLING DATE: NAME: US 07/827,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: NO. 5837822and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32744
TELECOMMUNICATION INFORMATION:
TELEPRONE: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
                                                                                                             73.8%;
78.1%;
                                                                                                  Query Match 73.85
Best Local Similarity 78.15
Matches 100; Conservative
; MOLÉCULE TYPE: protein
US-08-483-389-45
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Search completed: April 13, 2001, 15:36:11 Job time: 129 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein . protein search, using sw model

Run on:

April 13, 2001, 15:36:46

Search time 32.39 Seconds (without alignments) 297.043 Million cell updates/sec

US-08-700-737-15 757 Title: Perfect score:

MGWSCIILFLVSTATSVHSQ......DGWDYAIDYWGQGTSVTVSS 140 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

198801 seqs, 68722935 residues Searched:

198801 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	heavy chain	d heavy chain	d heavy	g meany chain pr	d heavy chain	d heavy chain	chain	g heavy chain	d heavy	heavy chain pr	d heavy chain pr	a heavy chain	d heavy chain	d heavy chain	d heavy chain	a heavy chain V	neavy	a heavy cha	a heavy chain	heavy chain	heavy cha	a heavy chain	a heavy	ene VH104B pro	heavy chain V	ntihody Fab Te	a heavy that	n heavy chain	chain	
Ω	E32513	MHMS18	JL0076	A30577	A27472	HVMST7	HVMS02	B47159	G2MS43	PL0208	E29380	F29380	JL0077	HVMS3	HVMS61	B22769	PH1482	HVMSG7	PS0024	S41394	HVMS23	MHMSB4	S21810	I84704	PH1489	S53751	HVMS45	A27609	A39276	
DB	7	7	~	~	~	٦		~		ď	N	~	~	Н	-	~	~	٦	ď	~	-	7	~	~	~	~	Н	~	~	
Length	138	139	141	135	131	. 138	117	136	137	136	137	137	136	117	117	120	140	140	139	120	117	117	138	116	140	116	117	139	141	
Query Match	79.7	79.2	78.3	9.9/	76.1	73.8	73.4	•			72.9		ď	÷	。	ö	ö		φ.	o.	σ.	6	o,	φ.	œ	8	8	æ		
Score			592.5		576	559	556	un .	554.5	Ŋ	551.5	2	5	543	ഗ	533.5	533	S	529.5	5	527	525	524	523	വ	519.5	519	518.5	517.5	
Result No.	н	~	m	4	ស	9	7	æ ·	o ,	10	11	13	13	14	12	16	17	18	19	20	21	22	57	24	52	56	27	28	53	

Ig heavy chain V r Ig heavy chain V r	pelB leader/Ig hea Ig heavy chain v	chain chain	chain chain	Ig gamma-2a chain Ig heavy chain v r	Ig heavy chain v I Ig pamma chain pre Ig heavy chain pre Ig heavy chain pre
PH1484 S20646	PC4402 S25175 PH1488	H32513 S20643	PH1493 PH1486 PH1498	S37483 PN0444 PH1492	A36194 S31930 S04575
77	400	000	7 77 77	9 9 9	0000
140	287 120 140	122	135 140 140	469 150	126 126 140
68.3 68.0	68.0	67.3	66.8 66.8	66.8 66.6	66.4 66.4 66.1
517 515	514.5 514 511	509.5	206 506 506	505.5 504.5 503	. 503 502.5 500
30	3 3 3 4	35	388	0 4 4 0 1 7 7	444 544

ALIGNMENTS

Gaps 5 Length 138; 79.7%; Score 603; DB 2; Length 13 82.9%; Pred. No. 2.6e-44; ive 7; Mismatches 15; Indels Query Match
Best Local Similarity 82.9
Matches 116; Conservative

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1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP ò g

61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120 δ

61 GGGLEWIGNIYPGSSSTNYNEKFKSKATLTVDTSSSTAYMQLSSLTSDDSAVYYCARRLY 120 qq

121 DGWDYAIDYWGQGTSVTVSS 140 ò q

RESULT MHMS18

Ig heavy chain precursor V region (B1-8) - mouse
N;Contains: Ig heavy chain precursor V region 186-2
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C;Accession: A90809; B90809; A22769; A02034; A02036
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies:

A; Accession: A90809

A; Molecule type: DNA A; Residues: 1-139 <B18>

A;Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115 A;Accession: B90809

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Decides Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-oct-1996
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-oct-1996
C;Accession: A27472
R;Liu, A.Y.: MacK, P.W.; Champion, C.I.; Robinson, R.R.
Gene 54, 33-40, 1987
A;Title: Expression of mouse::human immunoglobulin heavy-chain cDNA in lymphoid cells
A;Reference number: A27472; MuID:87277430
                                                                                                                                                                                                                                                                                                     Ig heavy chain precursor V region (MRL10) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996

C;Accession: A30577

R;Koffler, R; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th

J. Exp. Med. 161, 805-815, 1985

A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r

A;Reference number: A30577; MUID:85159423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;20-131/Product: Ig heavy chain V region 1E9 #status predicted <MAT>
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A; Residues: 1-131 < LIU>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Seywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 5-54/Region: complementarity.determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin homology
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pred. No. 4.7e-42;
4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 579.5; DB 2;
Pred. No. 2.5e-42;
8; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;34-117/Domain: immunoglobulin homology <IMM>F;69-85/Region: complementarity-determining 2 F;118-125/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; cross-references: GB:M37621
C; Superfamily: immunoglobulin V region; immunog
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 GYDGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AYWGOGTLVTVSA 135
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82.8%;
                                                                                                                                                     121 AG-----DYWGQGTTLTVSS 135
                                                                                                                           121 DGWDYAIDYWGQGTSVTVSS 140
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78.9%;
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Matches 111; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Status: preliminary
A Molecule type: mRNA
A; Residues: 1-135 <KOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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C; Species: Mus mu:culus (house mouse)
C; Accession: J1-Dec-19:11 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C; Accession: J100''6
R; Kaartinen, M.; Accea-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A; Title: Combinatorial association of V genes: one VH gene codes for three non-cross-real A; Reference numbe: J100''6
A; Molecule type: J100''6
A; Molecule type: J100''6
A; Molecule type: J100''6
A; Residues: 1-141 < KAAA.
A; Molecule type: DNA
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862
A; Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt A; Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
B; Didrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
BEMBO J. 1, 635-646, 1982
A; Title: Immunoglcbulin V region variants in hybridoma cells. II. Recombination between A; Reference number: A90971; MUID:84236026
A; Reference number: A90971; MUID:84236026
A; Residues: 20-135 < CDL>
A; Residues: 20-135 < CDL>
A; Residues: 20-135 < CDL>
A; Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch variant the mu chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GRGLEWIK;RIDPNSGGTKYNEKFKSKATLTYDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: hetercteramer; immunoglobulin
C; 19/20main: signal sequence #status predicted <SIG>
F; 20-139/Product: Ig kappa chain V region (B1-8) #status experimental *
F; 34-117/Domain: immunoglobulin homology <IMM>
F; 118-124/Region: D segment (JH2)
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Ig heavy chain procursor V region (anti-phenyloxazolone, 18C10)
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Pred. No. 2.1e-43;
7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 599.5; DB 1
Pred. No. 5.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
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80.0%;
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80.78;
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Best Local Similarity
Matches 112; Conserv
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Best Local Similarity
Matches 113; (onserv
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6

Indels

Length 135;

9 Gaps

5

Gaps

4

Length 131;

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RESULT 8
B47159
Igheavy chain V region, anti-carcinoembryonic maid T84.66 antigen monoclonal anti-id C; Species: Mus musculus (house mouse)
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C; Accession: B47159
R; Gaida, F.J.; Pleper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M. J. Biol. Chem. 268, 14138-14145, 1993
A; Title: Molecular characterization of a cloned idiotypic cascade containing a networ A; Reference number: A47159; MUID:93300804
A; Reference number: A47159; MUID:93300804
A; Status: preliminary
A; Molecular type: DNA; protein
A; Residues: 1-136 cGAI>
A; Experimental source: hybridoma 6G6.C4
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBIP:134422)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin
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A;Residues: 1-137 <BOT>
A;Cross-references: GB:J00539; NID:g195118; PIDN:AAA38172.1; PID:g195119
A;Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies
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C;Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (102) #status predicted
F:34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                          Length
                                                                                                                                     Score 556; DB 1; Le
Pred. No. 2.1e-40;
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                                                                                                                                                                                                           4; Mismatches
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89.78;
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Matches 106, Conservative
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A.Title: Illegitimate recombination generates a class switch from C-mu to C-delta in an A; Reference number: A02033; MUID:84248078
A; Accession: A02033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
C;Accession: A02032
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: A;Reference number: A90809; MUID:81234548
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A.Residues: 1-138 <GIL>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig heavy chain V region (TEPC 1017) #status predicted <MAT>
F:34-117/Region: V segment
F:34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 30-May-1997
C;Accession: A02033
                                                                                                                       GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                  Gaps
                                              MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
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A;Rosadues: 1-117 <BOT>
A;Note: the sequence was determined from the germline gene
A;Note: the germline gene, cloned from a library of strain C57BL/6 I (NPb antibodies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.8%; Score 559; DB 1; Length 138; 75.9%; Pred. No. 1.4e-40; tive 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain precursor V region (TEPC 1017) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain precursor V region (102) - mouse
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Best Local Simi
Matches 107;
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A; Residues: 1-137 <CHE>
A; Cross-references: GB:M17164; GB:J02815; NID:g195411; PIDN:AAA38295.1; PID:g195412
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (Labortalise)
C;Species: Mus musculus (Labortalise)
C;Accession: F29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J; Ribler: Nucleotide and translated amino acid sequences of cDNA coding for the A;Reference number: A92612; MUID:88007582
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C; Species: Mus pusculus (house mouse)
C; Decale: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C; Accession: JL0077
R; Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GQGLEWIGDIYPGSGSTNYNEKFKSKATLTVDTSSSTAXMQLSSLASEDSALXYCARQVG 120
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                                                               acid sequences of
      R.M.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 551.5; DB 2;
Pred. No. 5.8e-40;
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      A.; Ratcliffe,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; F
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino &
A;Reference number: A92612; MUID:88007582
A;Accession: E29380
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120 GNLWFA--YWGQGTLVTVSA 137
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77.9%;
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Best Local Similarity 75.09
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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A; Residues: 1-137 <CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Igheavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/C) (C;Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 20-Feb-1955 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998 (C;Accession: PLO28 # P. 1908 (C;Accession: PLO28 # P. 1908 (C;Accession: PLO27 # P. 1909 (C;Accession: PLO28 # P. 1909 (C;Accession: PLO20 * P. 1909 (C;Accession: P. 1909 (C;
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C;Species: Mus mus culus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: E29310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGLEWICEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQGLEWI(EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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                                                                                                         <MAT>
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                                                                                                                                                                                                                                                                                     Length 137;
                                                                                                  predicted
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            Superfamily: immunoglobulin V region; immunoglobulin homology
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         C; Superfamily: immunoglobulin V region; immunoylobulin C; Keywords: heterctetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F:10-137/Product: Ig heavy chain V region (543) #status | F;34-117/Domain: immunoglobulin homology <IMM>F;118-122/Region: J segment (JH2)
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                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                           Score 554.5; DB 1
Pred. No. 3.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
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74.1%;
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Best Local Similarity
Matches 106; Conserv
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Best Local Similarity
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Search completed: April 13, 2001, 15:36:47 Job time: 134 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 16/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily
                            RESULT
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                  A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A:Reference number: JL0076; MUID:89096973
A:Accession: JL0077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A02031
R; Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
A;Reference number: A90809; MUID: 81234548
A;Accession: A02031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V region (3) - mouse C:Species: Mus musculus (house mouse) C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A; Cross-references: GB:M27789; NID:g195853; PIDN:AAA38442.1; PID:g195854
A; Cross-references: GB:M27789; NID:g195853; PIDN:AAA38442.1; PID:g195854
A; Cross-references: GB:M27789; NID:g195853; PIDN:AAA38442.1; PID:g195854
A; Note: the authors translated the codon AGC for residue 114 as Arg
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F; 1-116/Domain: signal sequence (fragment) #status predicted <SIG>
F; 17-136/Product: Ig heavy chain #status predicted <MAT>
F; 17-51/Region: complementarity-determining 1
F; 18-136/Region: Omplementarity-determining 2
F; 118-136/Region: Usegment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-117 <BOY>
A; Note: the sequence was determined from the germline gene
A; Note: the germline gene, cloned from a library of strain C57BL/6 DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SCIMLFLAATATGVAKQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGKG
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(Signetics:
(Signetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-117/Product: IG heavy chain V region (3) #status predicted
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
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Pred. No. 2.6e-39;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 546.5; DB 2;
Pred. No. 1.5e-39;
7; Mismatches 17;
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88.0%;
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Best Local Similarity 77.4%;
Matches 106; Conservative
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Matches 103; Conservative
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Immunol. 25,
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Typeavy chain precursor V region (186-1) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 31-Mar-1989 #text_change 23-Aug-1996 C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 23-Aug-1996 C; Accession: D90809; Accession: B00809; MulD: Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore Cell 24, 625-637, 1981 A; Reference number: A0809; MulD: 81234548 A; Accession: D90809
                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-117 <BOT>
A;Note: the sequence was determined from the germline gene
A;Note: the 186-1 germline gene, cloned from a library of strain C57BL/6 DNA, belongs C;Genetics:
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F:20-117/Product: Ig heavy chain V region (186-1) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 117
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Pred. No. 8.3e-39;
5; Mismatches 13.
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ilarity 84.6%;
Conservative
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// Search time 21.32 Seconds
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                                                                                                                   1 MGWSCIILFLVSTATSVHSQ........DGWDYAIDYWGQGTSVTVSS 140
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P01771
            Compugen Ltd.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                  93435 seqs, 34255486 residues
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HV40_MOUSE
HV3J_HUMAN
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                                        OM protein - protein search, using sw model
                                                          April 13, 2001, 15:40:18
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Gapop 10.0 , Gapext 0.5
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757
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Maximum DB seq length: 200000000
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P06326 homo sapien
P01742 homo sapien
P01768 homo sapien
P01801 mus musculu
P01772 homo sapien
P01799 mus musculu
P60421 homo sapien
P01806 mus musculu
P01760 homo sapien
P01794 mus musculu
P01794 mus musculu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANDOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
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MEDLINE-81234548; Pubmed-6788376;
Bochwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION B1-8/186-2.
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Pest Local Similarity 80.7%; Pred. No. 2.4e-51;
Matches 113; Conservative 7; Mismatches 19; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
HV07_MOUSE
D HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
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D SEGMENT.
JH2 SEGMENT.
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                            HV1A_HUMAN
HV3G_HUMAN
HV32_MOUSE
HV3K_HUMAN
HV30_MOUSE
                                                                                                                                                    HV1H_HUMAN
HV36_MOUSE
HV1D_HUMAN
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HV27_MOUSE
HV25_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mushinski J.F.,
                      GQGLEWI( EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY
                                                                                              61 GRGLEWIC RIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY
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  MGWSCIII.FLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tucker P.W.;
"Illegitimate recombination generates a class switch from C mudelte in an ign-secreting plasmacytoma.";
Proc. Natl. Rcad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
Interpro: IPP003006; -.
Pfam: PF00047; ig: 11.
Immunoglobulin V region; Signal.
SIGNAL.
21 138 IG HEAVY CHAIN V REGION TEPC 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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COMPLEMENTARITY-DETERMINING 1.
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COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=8424£078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                              23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                            138 AA
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HV06_MOUSE
1D HV06_MOUSE STANDARD; F
AC PO1750;
DT 21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                           121 YGSSY-FIYWGQGTTLTVSS 139
                                                                                                                                                       DGWDYAIL YWGQGTSVTVSS 140
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138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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P03980;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                        Baltimore D.;
"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell.24:625-637(1981)
-1- MISCELLANEOUS: THIS GERMIINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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                                                                                                                                                                                                                                                        MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies: somatic mutation evident in a gamma 2a variable region." cell 24:625-837(181).
-!- MISCELLANBOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION 102.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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89.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6;
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                                                                                                                                                     NCBI_TaxID=10090;
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117
117 ;
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                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                           GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR--- 117
                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                73.2%; Score 554.5; DB 1; Length 137; 74.1%; Pred. No. 5.4e-47; ative 9; Mismatches 19; Indels 9,
                                                                                                                                                       FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                              FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                             HEAVY CHAIN V REGION S43
                                                                                                                                                                                                                                                             15200 MW; ADD5881BF44B8EC9 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 3 PRECURSOR.
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                                                                    EMBL; J00539; AAA38172.1; -. PIR: A02038; GZMS43. Interpro; IPER030306; -. Pfam: PF00047; ig; l. Immunoglobulin V region; Sign
                                                                                                                                                                                                                                                                                                           Best Local Similarity 74.1
Matches 106; Conservative
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137 AA;
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AC P01749;
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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                       COMPLEMENTARITY - DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                     Length 117;
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                                                                                                                                                                                                                                                                                                            71.7%; Score 543; DB 1; Length 11
88.0%; Pred. No. 5.9e-46;
....matches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                     IG HEAVY CHAIN V REGION 3.
                                                                                                                                                                                                                                                                          MW; 427C861C53975EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 537; DB 1;
Pred. No. 2.2e-45;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV09_MOUSE STANDARD: PRT; 117 AA. AC. B HV09_MOUSE STANDARD: PRT; 117 AA. AC B HV09_MOUSE STANDARD: BT 21-JUL-1986 (Rel. 01, Created) DT 01-JUL-1989 (Rel. 11, Last sequence update) DT 01-JUL-1999 (Rel. 138, Last annotation update) DE 15-JUL-1999 (Rel. 138, Last annotation update) DE 1G HEAVY CHAIN V REGION 186-1 PRECURSOR.
                                                                                                                                                                                                                                    BY SIMILARITY.
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MEDLINE=81234548; PubMed=6788376;
EMBL; J00536; AAA38605.1; -.
PIR; A02031; HVMS3.
InterPro; IPR003006; -.
Fam; PF00047; 1g; 1.
Immunoglobulin V region; Signal.
SIGNAL.
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InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region; Signal.
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84.6%;
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Best Local Similarity 88.03
Matches 103; Conservative
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Best Local Similarity 84.6
Matches '99; Conservative
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115
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117 AA;
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HV02_MOUSE

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                                                                                                                                                                                                                              Baltimore D.; "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).

-I- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GOGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMOLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 527; DB 1;
Pred. No. 2.1e-44;
3; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
Mus musculus (Mouse).
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION 23 PRECURSOR.
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                                                                                                                                                                                            MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin V region; Signal.
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83.8%;
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InterPro; IPR003006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
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Matches 98; Conser
                                                                                                                                                       SEQUENCE FROM N.A.
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P06328;
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SEQUENCE
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                    1 MGWSCII.JFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                   1 MGWSFIFLFLLSVTAGVHSEVQLQOSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP
                                                                                               61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                            21-JUL-1986 [Rel. 01, Created)
21-JUL-1986 [Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
BURS muscalus (Mouse).
Eukaryota; Matazaa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eu.heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID-1)090;
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                            1 MGWSCIM.FLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWWHWVKQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.3%; Score 532; DB 1; Length 140;
.larity 72.1%; Pred. No. 8.4e-45;
Jonservative 11; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Somatic mutition in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15514 MW; 25A4CBBE31DA5CE8 CRC64;
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MEDLINE=82152818; Pubmed=6801765;
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ID HV04_MOUSE STANDARD;
AZ P01748;
DT 21-JUL-1986 (Rel. 01, Created)
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Best Local Similarity
Matches 101; Jonserv
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P01746;
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 117
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B8862FAC67ABD345 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 117 AA. P11270; PRT; 117 AA. P1754; P11270; P1754; P11270; P1754; P1750; P1751, P1750; P1751, P17511, P1751, P1751, P1751, P1751, P1751, P1751, P1751, P1751, P17511, P175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK 2
                                         email to license@isb-sib.ch)
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or send a..

EMBL, M13788; AAA30-
PIR; A020335, MHMSB3.

JR InterPro; IPP003006; -
FT CHAIN 20 117
FT CHAIN 20 117
FT COMAIN 50 54 CO
DOMAIN 50 68 FRA'
FT COMAIN 50 68 FRA'
FT CHAIN 50 6
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Immunoglobulin V region; Signal.
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Matches 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit thattutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announced or send an email to license@lab.sib.ch).
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                  1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes."

Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S. Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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8
    FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.7%; Score 497; DB 1; Length 136; 68.3%; Pred. No. 2e-41; ive 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION BCL1.
                                                                                                                                                          68.6%; Score 519; DB 1; Length 11
82.9%; Pred. No. 1.2e-43;
Live 5; Mismatches 15; Indels
                                                                                              MW; D37DE8A3F543E996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION BCL1 PRECURSOR,
                                                  FRAMEWORK 3.
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MEDLINE-82222262; PubMed-6806821;
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J00494; AAA38130.1; -.
68
85
117
117
12921 1
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Best Local Similarity 82.99
Watches 97; Conservative
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Best Local Similarity
Matches 97; Conserv
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P01759;
                     DOMAIN
DOMAIN
NON_TER
SEQUENCE
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21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
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P01756;
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MEDLINE-83131846; PubMed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Bur. J. Immenol. 12:1023-1032(1982).
                                                                                                                                                                                                      MEDLINE—8418:519; PubMed—6201362;
Dildrop R., Hovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
Dildrop R., Hovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
M. V region (eterminant (idiotope) expressed at high frequency in B Lymphocytes :s encoded by a large set of antibody structural genes.";
EMBO J. 3:51:-523(1984).
PIR; A02037, MHMS15.
IntherPro; IPH:003006;
-.
Pfam; PF:0004'; ig: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
16 HEAVY CHAIN V REGION 36-65.

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Actazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; MuscallaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                           20 OVQLQQP;AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                    63.3%; Score 479.5; DB 1
75.2%; Pred. No. 8.4e-40;
iive 7; Mismatches 22
                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEWY CHAIN V REGION AC38 15.3.
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D SEGMENT.
J SEGMENT.
BY SIMILAR?
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               119 GYDGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.3
Best Local Simi arity 75.2
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                              STANDARD;
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22
..20
130 AA;
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P01747;
                                                                           HV50_MOUSE
P06329;
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NON_TER
SEQUENCE
                                                                                                                                                                                               SEQUENCE
                        121 NY
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                                                        RESULT 12
HV50_MOUSE
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Biochemistry 21:5415-5424(1982).
-!- MISCELLANGOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYCAR----DYDWYFDVWGAGTTVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TO THE SAME
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                  21 VOLOOPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKORPGQGLEWIGEIDPSESNTNYN 80
                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Complete amino acid sequence of a mouse mu chain: homology among
  OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE.
MEDLINE-83075344; PubMed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                          ; Score 468; DB 1; Length 120;
; Pred. No. 1.1e-38;
10; Mismatches 21; Indels
                                                                          SEGMENT, JH2.
PIR: A02028; HYMSG7.
InterPro; IPR00306; -.
Pfam; PF00047; 19:1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
-i- MISCELLANDOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL ODIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                           120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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71.1%; Pred. No. 1.1e-36;
:ive 12; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01, Last sequence update)
38, Last annotation update)
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InterPro; IPR003006; -.
Ppfam, P0047; ig: 1.
Immunoglobulin V region; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION MOPC 104E. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                   61.8%;
74.2%;
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 74.2%
Matches 89; Conservative
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Best Local Similarity 71.1<sup>1</sup>
Matches 86; Conservative
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Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
- INSCELLANDEDS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOMA THAT SECRETES IGG2B.
DIR; A02027; GVMS11.
InterPro; IRRO03006; -
Pfam; PF00047; ig; 11.
Immunoglobulin V region.
NON_TER 121
SEQUENCE 121 AA: 13135 MW; 227AEF3EC56ED0BF CRC64;
HV01_MOUSE STANDARD; PRT; 121 AA.
P01745;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HRAYY CHAIN V REGION MPC 11.
Mus musculus (Mouse).
Musmalla; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MCBI_TaxID=10090;
WCBI_TaxID=10090;
                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-8105371; PubMed-6253904;
Zakut R., Cobs71; Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPCII.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 59.0%; Score 447; DB 1; Length 121; Best Local Similarity 69.4%; Pred. No. 1.2e-36; Matches 84; Conservative 12; Mismatches 25; Indels
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Search completed: April 13, 2001, 15:40:19 Job time: 272 sec

20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGGGLEWIGEIDPSESNTNY 79

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2001, 15:39:54; Search time 56.51 Seconds

(without alignments)
290.375 Million cell updates/sec

Perfect score: 757
Sequence: 1 MGWSCILLFLVSTATSVHSQ......DGWDYAIDYWGQGTSVTVSS 140

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL.15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mamman:*
7: sp_mhc:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_noclassified:*
11: sp_rocent:*
11: sp_rocent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_vertebrate:*
14: sp_vertebrate:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery No. Score Match Length DB ID

1 473 62.5 117 11 090XE9
2 464.5 61.4 110 11 091Z7
3 462.5 61.1 114 11 091Z7
4 459 60.6 118 11 091Z7
4 473 57.7 117 11 090XE0
6 42.8 5 60.6 118 11 091Z7
7 437 57.7 117 11 091Z76
9 414.5 54.8 124 4 091Z94
10 412.5 54.8 124 4 091Z94
11 404 53.4 150 11 091Z163
12 396 51.0 19 11 091Z163
13 366 51.0 19 11 091Z163
14 386 51.0 19 11 091Z163
15 356.5 47.1 116 4 091Z163
16 356.5 47.1 116 4 091Z163
17 323 42.7 116 4 091Z163
18 313.5 41.4 147 4 091Z90
19 313.5 41.4 147 4 091Z90
19 313.5 41.4 147 4 091Z90
10 091Z90
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RESULT

09u191 homo sapten 09u188 homo sapten 09u188 homo sapten 09u171 homo sapten 09u172 homo sapten 09u172 homo sapten 09s973 homo sapten 09s973 homo sapten 09u186 homo sapten 09u187 homo sapten 09u187 homo sapten 09u196 homo sapten 07573 homo sapten 07574 homo sapten	0/5/28 homo sapien
090L91 090L81 090L81 090L72 090L73 090L73 095773 095773 090L86 090L86 090L86 090L87 090L87 090L74 075729 075729 075729	04/0/0
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ALIGNMENTS

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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characteri.ation of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucksamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; APZO60425, AAF69323.1; -.
NON TER 1 1
                                                                                                                                                       STRAIN=DBA/2.
Malkiel S., Jaco L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-gluco;amine antibodies from mice with autoimmune myocarditis.";
Submitted (NYV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF206019; AAF69237.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 LVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKATL 89
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                01-0CT-2000 TrEMBLrel. 15, Created)
01-0CT-2000 TrEMBLrel. 15, Last sequence update)
01-0CT-2000 TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN ::MMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                Mus musculus (Mouse).
Eukaryota, Matazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eucheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 LYVDKS3STAYMQLSSPTSEDSAVYYCARSNYYGSSLYYFDYWGQGTTLTVSS 114
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Pred. No. 3.7e-40;
; Mismatches 17; Indels 1;
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                                                                                                                                                                                                                                                                                    DB 11; Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                             12829 MW; 404885FDE6BA56F8 CRC64;
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           110 AA.
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larity 77.9%;
Conservative
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          PRELIMINARY;
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Best Local Sim.larity
Matches 88; Conserv
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Matches 88; Conserv
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                                                                                                                    NCBI_TaxID=1,090;
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             Q9JL77
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Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P., Matis L.M., Evans M.J.;
Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/64 constant regions block human leukocyte binding to porcine endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKGKATLIVDKSSSTAYMQLNSLISEDSAVYYCARDK----DYYFDYWGQGTTLIVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 139
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEWBLrel. 10, Last sequence update)
01-MAY-2000 (TrEWBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRACMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                            Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ255171; CAB65236.1; -
INTERPRO; IPR003006; -
PFAM; PF00047, 19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           13060 MW; D816AD0858A47E4C CRC64;
01-MAY-2000 (TrEMBLrel. 13, Créated)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.6%; Score 459; DB 11; 72.7%; Pred. No. 8.7e-40; ive 11; Mismatches 18;
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11; Mismatches
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117 AA;
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Best Local Similarity
Matches 88; Conserv
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Length 118;

DB 11;

Score 458.5;

60.68;

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NCBI_TaxID=9606;
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Malkiel S., Lidao L., Cunningham M.W., Diamond B.;
"Characterization of cross reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF206031; AAF205391; -.
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STRAIN-BALB/C;
Mueller J.P., Glannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Mueller J.B., Evans M.J.;
Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric
1962/64 constant regions block human leukocyte binding to porcine
                                                                                                                                                          80 NOKFKGKATLIVDISSSTAYMQLSSLTSEDŠAVYYCAR---GGYDGWDYAIDYWGQGTSV 136
                                                                                                                                                                                     61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGY-----FDYWGQGTTL 114
                               Gaps
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                                                                        QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0921C6; 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 442.5; DB 11; Length 109; 76.1%; Pred. No. 3.9e-38; 11ve 8; Mismatches 14; Indels 5;
  9.8e-40;
ches 18; Indels
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  71.8%; Pred. No. 9.8e
Best Local Similarity 71.8 Matches 89; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                         137 TVSS 140
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JL75
Q9JL75;
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Q9JL75
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01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                              20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGPQLVRPGTSVKISCKASGYSFTSYWMHWVKQRPGQDLEWIGMIDPSDSEVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e
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                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.5%; Pred. No. 3.4e-35;
Matches 80; Conservative 17; Mismatches 24; Indels
                                 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         13122 MW; 4F65B193AFB77E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                    Query Match 57.7%; Score 437; DB 11; Best Local Similarity 70.2%; Pred. No. 1.6e-37; Matches 85; Conservative 8; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AF035022; AAD56258.1; -.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98277139; PubMed=9614934;
endothelial cells.";
Submitted (NOV-1996) to the
EMBL; U78799; AAD00291.1; -.
INTERPRO; IPR003006; -.
PFAM; PF00047; 1g; 1.
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                                                                                                                                                           117 1
117 AA;
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01-MAY-2000 (T.EMBLrel. 13, Last sequence update)
01-JUN-2000 (T.EMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GQGLEWIGEIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9832155; PubMed-9657749;
Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and Kinetics of factor VIII inactivation: study with an
IgG4 monoclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
                       2 ELVKPGASVKISCKASGYTFSNSWANWVKLRPGQGLEWIGRIYPGDGDAYYNGKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                       89 LTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 140
                                                                                                                 53.4%; Score 404; DB 4; Length 150; 56.4%; Pred. No. 5.2e-34; ive 17; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-98277139; Pubwed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M..
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 POTENTIAL.
150
16031 MW; 563D164AB22802D5 CRC64;
                                                                                                                                                                                                                                                                                              01-NoV-1999 (TrEMBLrel. 12, Created)
01-NoV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                                                                                                                                                IGG VH PROTEIN PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DGWDYAIDYWGQGTSVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 D----AFDIWGQGTMVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibitor.";
Blood 92:496-506(1998).
EMBL; AJ224083; CAA11829.1;
INTERPRO; IPRO03006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.44
Matches 79; Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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SIGNAL
NON_TER
SEQUENCE
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Q9Y298;
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                                                                                                                                                                                                      RESULT 11
Q9Y298
    29
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"Characteriz.tion of cross-reactive monoclonal anti-myosin/anti-n-acetyl-gluco:annine antibodies from mice with autoimmune myocarditis.";
Submitted (NYV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206013; AAF69321.1; --
NON_TER
                                                                  01-MAY 2000 TrEMBLrel. 13, Created)
01-MAY 2000 TrEMBLrel. 13, Last sequence update)
01-MAY 2000 TrEMBLrel. 14, Last annotation update)
01-JUN-2000 TrEMBLrel. 14, Last annotation update)
MYOSIN-REACT:VE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; M:tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NQKFKGK.VILIVDISSSTAYMQLSSLISEDSAVYYCARGGYDG-WDYAIDYWGQGTSVTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLQQP/AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN (MMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eu:heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=1)090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÷
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                                                                                                                                                                                                                                                                                                                     Wu X., Liu B , Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.7%; Score 414; DB 4; Length 119; 65.6%; Pred. No. 3.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12052 MW; 84E6F2AD219AF95E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1... 9 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.5%; Score 412.5; DB 1 70.5%; Pred. No. 4.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immuno... Immunopathol. 87:184-192(1998).
EMBL; AF0350:0; AAD56256.1; -...
INTERPRO; IPN003006; -...
PFAM; PF0004"; ig: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches
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                            119 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                              PRT;
                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=9827''139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi.arity 65.69
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELIMINARY;
                              'RELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
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                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best*Local Simi
Matches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 SS 140
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NON_TER
SEQUENCE
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SEQUENCE
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                                                    09UL94
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         Q9UL94
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 JOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M., Bohlen H., Diehl V., Wolf J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated with somatic mutations within the untranslated regions of rearranged and
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGG-
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 'Myosin-reactive autoantibodies in rheumatic carditis and normal
 Length 116;
 51.0%; Score 386; DB 4; Length 157; ilarity 51.4%; Pred. No. 3.9e-32; Conservative 24; Mismatches 35; Indels
 SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
WU X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
Young D.C.;
 Indels
 class switch recombinated Ig genes."
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AA005570; CAA06599.1; -.
INTERPRO; IFRO3006; -.
PFAM: PF00047; ig; 1.
 1 21 POTENTIAL.
157 157
157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
 C8F9131DE13EA898 CRC64;
 DB 4;
 29;
 47.1%; Score 356.5; DB 4
60.3%; Pred. No. 2.8e-29;
11ve 16; Mismatches 29
 fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035025; AAD56261.1; -.
PTREPRO; PR003066; -.
PFAM; PF00047; ig; 1.
 116 AA.
 120 ----YDGWDYAIDYWGQGTSVTVSS 140
 PRT;
 PROTEIN PRECURSOR (FRAGMENT)
 116 AA; 12605 MW;
 Query Match 47.1
Best Local Similarity 60.3
Matches 70; Conservative
 SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
 PRELIMINARY;
 116
 Local Similarity
es 75; Conser
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 NON_TER
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 Query Match
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 Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF206021; AAF69319.1:
 Gaps
 80 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCAR----GGYDGWDYALDYWGQGTS 135
 :III : III: III III:III | IIII | IIII | IIII | IIIII | IIIII | III | IIII | III | II
 20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
 Gaps
 28 AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKA 87
 01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
'Myosin-reactive autoantibodies in rheumatic carditis and normal
 4 ;
 88 TLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSVTVSS 140
 61 TITSDISSNIAYLOLSSLISEDTAVYYCVRRG----AVVFDYWGQGTALIVSS 109
 51.0%; Score 386; DB 11; Length 109; 64.6%; Pred. No. 2.5e-32;
 Length 125;
 Query Match 51.5%; Score 390; DB 4; Length 12
Best Local Similarity 60.0%; Pred. No. 1.1e-32;
Matches 75; Conservative 16; Mismatches 30; Indels
 Indels
 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;
 Created)
Last sequence update)
Last annotation update)
 23;
 fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL: AF035019; AAD56255.1; -.
INTERPRO; IPR003006; -.
 Best Local Similarity 64.6%; Pred. No. 2.5e-Matches 73; Conservative 13; Mismatches
 109 AA
 157 AA
 PRT;
 PRT;
 095978;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-2000 (TrEMBLrel. 13,
 PRELIMINARY;
 PRELIMINARY;
 PFAM; PF00047; 1g; 1
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090
 121 VTVSS 125
 136 VTVSS 140
 STRAIN-BALB/C
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SEQUENCE
 NON_TER
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 Query Match
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09JL85 **09JL85** 

RESULT 13 Q9JL85

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RESULT 095978

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QY Db

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Search completed: April 13, 2001, 15:39:54 Job time: 266 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

April 13, 2001, 15:35:39 ; Search time 57.59 Seconds (without alignments) 138.963 Million cell updates/sec

US-08-700-737-15 757 1 MGWSCIILFLVSTATSVHSQ......DGWDYAIDYWGQGTSVTVSS 140 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

390729 seqs, 57163235 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

\*\*SIDSI./gcgdata/geneseq/geneseqp/AA1980.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1986.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:\*

\*\*SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1980.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1990.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1991.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1991.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1991.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1991.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/AA1991.DAT:\*

\*\*SIDSI/gcgdata/geneseqp/geneseqp/AA1991.DAT:\*

\*\*SIDSI/gcgdata/geneseqf/geneseqp/AA1995.DAT:\*

\*\*SIDSI/gcgdata/geneseqf/geneseqp/AA1995.DAT:\*

\*\*SIDSI/gcgdata/geneseqf/geneseqp/AA1996.DAT:\*

\*\*SIDSI/gcgdata/geneseqf/geneseqp/AA1999.DAT:\*

\*\*SIDSI/gcgdata/geneseqf/geneseqp/AA2000.DAT:\*

\*\*SIDSI/gcgdata/geneseqf/geneseqp/AA2000.DAT:\* A\_Geneseq\_0401:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. the number of Pred. No.

|        |       | ,     |                    |     | SUMMARIES                               |                          |
|--------|-------|-------|--------------------|-----|-----------------------------------------|--------------------------|
|        |       | æ     |                    |     |                                         |                          |
| Result |       | Query |                    |     |                                         |                          |
| NO.    | Score | Match | Match Length DB ID | DB  | ID                                      | Description              |
|        |       |       |                    |     | ******************                      |                          |
| -      | 757   | 100.0 | 140                | 19  | W53815                                  | Wiring Act-1 bearing     |
| ~      | 730   | 96.4  |                    | 10  | W53818                                  | Dantel Act I Heavy       |
|        |       |       |                    | 1   |                                         | . Protein seduence o     |
| •      | 113   | 74.2  |                    | 19  | W53816                                  | Consensus protein        |
| 4      | 632   | 83.5  |                    | 6   | W53813                                  | Toping phase of          |
| u      | 1     |       |                    | 1   |                                         | neavy chain or a n       |
| n      | CTO   | 81.2  |                    | 13  | W83041                                  | Anti-Fas MAN HEF7A       |
| 9      | 615   | 81.2  |                    | 2   | 71777 B                                 | WITH OWN CO. TOWN        |
|        |       | 1 7   |                    | 4 1 | 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 | Mouse anti-Fas ant       |
| _      | CT0   | 81.2  |                    | 7   | M90897                                  | Miring anti-Eas an       |
| œ      | 597   | 78.9  |                    | 4   | 076090                                  | יימי דווי מוורד דמים מוו |
|        | 1     |       |                    | 7   | 000074                                  | MAD 55.1 heavy cha       |
| ת      | 3.4.5 | 78.5  |                    | 18  | W24025                                  | Single chain antio       |
| 10     | 289   | 77 8  |                    |     | 0707040                                 | היים ביים ביים מוורדם    |
| ) , i  | 9 6   |       |                    | î   | K2/049                                  | VH425 antibody clo       |
| 11     | 280   | 7.7.4 |                    | ထ   | P70624                                  | Sequence encoded h       |
|        |       |       |                    |     |                                         | 1 101100000              |

| epatiti<br>human c<br>ic anti<br>anti-he<br>anti-he | Chimeric anti-hopa<br>MAb SCH94.03 heavy<br>Humanised anti-Fas<br>Humanised anti-Fas<br>Anti-Fas Mumanised<br>Humanised anti-Fas | sed HEETA dised anti-Fa ant of human ise anti-Fa as humanise as humanise as humanise sed anti-Fa sed HEETA d | MAD 2E12<br>chain var<br>acid sequ<br>ric anti-<br>onal anti-<br>variable | pot-nl protein pro<br>MAD Co-1 heavy cha<br>Mouse Co-1 heavy cha<br>Anti-DNA antibody<br>Co-1 Heavy Chain v<br>Anti-tobacco mosai<br>Anti-EGFR antibody |
|-----------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| W10584<br>W16340<br>W10239<br>W47510<br>W41054      | W89535<br>R84554<br>W90933<br>W90934<br>W83037<br>B14779                                                                         | W90929<br>W90935<br>W81775<br>W90925<br>W83036<br>B14776                                                     | R12233<br>R12355<br>W50218<br>B08026<br>W44177<br>R95215                  | KZ2003<br>W865213<br>W85661<br>W07436<br>R09425<br>R66758                                                                                               |
| 119                                                 | 20<br>21<br>21<br>21<br>21<br>21<br>21                                                                                           | 221 221 221 221 221 221 221 221 221 221                                                                      | 777777777777777777777777777777777777777                                   | 18<br>18<br>11<br>16<br>16                                                                                                                              |
| 136<br>136<br>136<br>136                            | シキレレレレ                                                                                                                           | 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                      | 143<br>144<br>138<br>140<br>140                                           | 0 <del>4 4 4 4 6 4</del>                                                                                                                                |
| LLLLLLL                                             |                                                                                                                                  | 2.44.44.44.44.44.44.44.44.44.44.44.44.44                                                                     | ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~                                   | :::::::::::::::::::::::::::::::::::::::                                                                                                                 |
|                                                     | . വെയയയ                                                                                                                          | , വ വ വ വ വ വ വ വ                                                                                            |                                                                           | 36.334                                                                                                                                                  |
| 112<br>113<br>114<br>116                            | 22<br>22<br>23<br>23<br>23                                                                                                       | 22222222222222222222222222222222222222                                                                       | 7 M M M M M M M M M M M M M M M M M M M                                   | ) 4 4 4 4 4<br>) 0 11 0 12 8 4 8                                                                                                                        |

## ALIGNMENTS

RESULT

Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease. Murine Act-1 heavy chain variable region. Location/Qualifiers W53815 standard; Protein; 140 AA. (first entry) 14-JUL-1998 Peptide W53815; Mus. sp. Key W53815 

/note= "signal peptide" 20.140 /note= "mature protein" Protein

WO9806248-A2

19-FEB-1998.

97WO-US13884. 06-AUG-1997;

96US-0700737. 15-AUG-1996;

(LEUK-) LEUKOSITE INC.

```
Misc-difference 6
 14-JUL-1998
Saldanha J;
 Sequence
 Query Match
 61
 Mus
 RESULT
W53816
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 0
 The present sequence represents the heavy chain varaible region of murine antibody Act-1. Act-1 is active against human alpha4-betta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of th.s particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a light of crapha4-beta7. It can be used for inhibiting diseases such as inflammatory bowel diseases. The immunoglobulin can also be used for detection, isolation and diagnosis.
 Protein sequence of murine variable heavy chain region of clone H2B#34
 61 ggglewijeldpsesntnyngkfkgkatltvdissstaymqlssltsedsavyycarggy 120
 61 GOGLEWI BEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Gaps
 9
 1 MGWSCIIJELVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Mouse; Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; Mumanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
 Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for trecting inflammatory disease, pancreatitis, diabetes, asthma, graff versus host disease and sarcoidosis
 ;
 Length 140;
 Ringler DJ;
 Indels
 Ringler DJ;
 Score 757; DB 19;
Pred. No. 2.4e-55;
0; Mismatches 0;
 Ponath PD,
 Ponath PD,
 Newman W,
 AA
 Newman W,
 Claim 27; Fig. 9; 145pp; English
 100.0%;
100.0%;
 W53818 standard; Protein; 137
 .21 DGWDYALJYWGQGTSVTVSS 140
 121 dgwdyailywgggtsvtvss 140
 97WO-US13884
 96US-0700737
 (first entry)
 Best_Local Similarity 100.
Matches 140; Conservative
 Jones ST,
 (LEUK-) LEUFOSITE INC
 ST,
 WPI; 1998-159172/14.
N-PSDB; V20078.
 1.10 AA;
 cones
 06-AUG-1997;
 15-AUG-1996;
 WO9806248-AZ
 14-JUL-1998
 19-FEB-1998
 Bendig MM,
 Saldanha J;
 Σ
 Sequence
 Query Match
 W53818;
 Mus sp
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 W53818
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ó
 The present sequence represents the amino acid sequence comprising the variable region of murine Act-1 antibody determined from clone H2B#34. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin call adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The present sequence was used to construct chimeric. The humanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of calls bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Consensus protein sequence of the murine variable heavy chain region.
 Gaps
 Mouse: Act-1 antibody; human alpha4-beta7 integrin; Muscosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; inflammatory disease; inflammatory bowel disease.
 integrin
diabetes,
 ó
 Length 137;
 Indels
 encoded by RRA"
 'note= "not specified, encoded by TRK"
 Humanised immunoglobulin reactive with alpha-4-beta-7 used for treating inflammatory disease, pancreatitis, asthma, graft versus host disease and sarcoidosis
 encoded by
 Score 730; DB 19;
Pred. No. 3.9e-53;
 Mismatches
 note= "not specified,
 specified,
 'note= "not specified,
 Location/Qualifiers
 W53816 standard; Protein; 144 AA.
 Example 1; Fig 2; 145pp; English.
 "not
 96.4%;
llarity 98.5%;
Conservative
 (first entry)
 121 DGWDYAIDYWGQGTSVT 137
 /note=
WPI; 1998-159172/14.
 Best Local Similarity
Matches 135; Conserv
 137 AA;
 Misc-difference 5
 Key
Misc-difference
 Misc-difference
 Misc-difference
 N-PSDB; V20089.
```

m

by YTC"

region 3"

"CDR2"

"CDR1"

```
'note= "not specified, encoded by RTC'
 'note" "not specified, encoded
 131..141
/note= "framework region 4"
 20..49 // framework region 1"
 55..68
/note= "framework region 2"
 note - "encoded by ATY"
 /nocc
86..117
`-+≏= "framework r
 118..130
/note= "CDR3"
 96US-0700737.
 97WO-US13884
 69..85
/note=
 note-
 (LEUK-) LEUKOSITE INC.
 Jones ST,
 WPI; 1998-159172/14.
 144 AA;
 Misc-difference
 Misc-difference
 N-PSDB; V20085.
 WO9806248-A2
 06-AUG-1997;
 15-AUG-1996;
 19-FEB-1998
 Saldanha J;
 Bendig MM,
 Pept1de
 Protein
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 Region
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 Region
 Reg 1on
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The present sequence tepresents the Conscissor acts sequence.

Comprising the variable region of murine Act-1 antibody determined from several independent mouse heavy chain variable region clones. Act-1 is active against human alpha+ beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadcAm-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha+ beta7 integrin binding to MadCAm-1, which is present of high endothelial venules in mucosal by machine and sequence. The present sequence consensus sequence. The present sequence was used to construct chamanised Act-1 antibodies, which contain murine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha+ beta7 with cells bearing a construct contain of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel diseases. The immunoglobulin can also be used for alpha+ beta7. It can be used for inhibiting leukocyte as inflammatory bowel diseases. The immunoglobulin can also be used for an animal and the immunoglobulin can also be used for an animal anim
 The present sequence represents the consensus amino acid sequence
 Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
Ponath PD, Ringler DJ;
 detection, isolation and diagnosis.
3
 Example 1; Fig 1; 145pp; English.
Newman
```

Gaps .; 0 DB 19; Length 144; Indels 1; Score 713; DB 19 Pred. No. 1e-51; 0; Mismatches 94.2%; Query Match
Best Local Similarity 99.3°
Matches 133, Conservative

```
The present sequence represents the heavy chain of humanised murine antibody Act-1. Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for detection, isolation and diagnosis.
 99
 Mouse; Act-1 antibody; human alpha4-beta7 integrin; wascosal adressin cell adhesion molecule-1; MadCAM-1; humanised antibody; murine antigen binding region; inhibition; leukocyte infiltration of tissue; treatment; infiammatory disease;
IGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYA
 Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes asthma, graft versus host disease and sarcoidosis
 Ringler DJ;
 Heavy chain of a humanised murine Act-1 antibody.
 Ponath PD,
 /note= "signal peptide"
20..180
/note= "mature protein"
 "mature protein"
 Location/Qualifiers
 W53813 standard; Protein; 180 AA.
 Newman W,
 Claim 20; Fig 11; 145pp; English.
 97WO-US13884
 96US-0700737
 inflammatory bowel disease
 (first entry)
 127 IDYWGQGTSVTVSS 140
 Jones ST,
 (LEUK-) LEUKOSITE INC
 WPI; 1998-159172/14.
N-PSDB; V20076.
 WO9806248-A2.
 Mus sp.
Homo sapiens
 06-AUG-1997;
 14-JUL-1998
 15-AUG-1996;
 19-FEB-1998.
 Saldanha J;
 Sendig MM,
 Synthetic.
 Peptide
 Protein
 W53813;
 29
 RESULT
W53813
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180 AA;

Sequence

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(SANY) SANKYO CO LTD.
 24-NOV-2000
 Mus musculus
 Akio S, Hid
Masahiko O,
 Sequence
 B14747;
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 RESULT
B14747
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 .;
0
 Gaps
 65
 6 IILFLVS1 ATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLE
 apoptosis; HIPDA, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; Siogrem syndiome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid a:thritis; autoimmune haemolytic anaemia; myasthenia g:avis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atoricosclerosis; myocarditis; cardiomyopathy; glomerular niphritis; hypoplastic anaemia; hepatitis; AIDS; transplant rijectlon; therapy; complementarity determing region;
 ;
 Length 180;
 monoc.onal antibody; mouse; Fas; humanised antibody;
 83.5%; Score 632; DB 19;
85.9%; Pred. No. 5.8e-45;
iive 9; Mismatches 10;
 1.19
/label= Sig_peptide
 20..464
/label= Mat_protein
 Location/Qualifiers
 /label= Variable
 W83041 standard; Protein; 464 AA
 /label= Constant
 'note= "claim 9"
 /note= "claim 9"
 /note= "claim 9'
 Anti-Fas MAb HFE7A heavy chain.
 59..84
/label= CDR_H2
 50..54
/label= CDR_H1
 CDR_H3
 97JP-0276064.
97JP-0082953.
97JP-0169088.
 98AU-0059701
 (first entry)
 118..128
/label= C
 Matches 116; (onservative
 126 AIDYWGQCTSVTVSS 140
 ..464
 .140
 Similarity
 08-OCT-1997;
01-APR-1997;
25-JUN-1997;
 30-MAR-1998;
 Mus musculus
 15-MAR-1999
 AU9859701-A
 08-OCT-1998
 Query Match
Best Local S
 Peptide
 Protein
 W83041;
 Region
 Region
 Region
 Region
 Region
 RESULT
 W8304
 Dp
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```
This is the amino acid of the heavy chain of murine anti-human Fass monoclonal antibody HFE7A. CDNA (see V70129) encoding the heavy chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828).

CRNA by RT-PCR (see V70125-26). The invention provides humanised HFE7A antibodies (see W83031-37) produced by CDR grafting. These antibodies are capable of inducing apoptosis in abnormal cells. Capressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus cauch diseases, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, calcroderma, Goodpasture syndrome, Crohn's disease, rheumatoid gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, dimerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
 61. GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 61 ggglewigeidpsdsytnyngkfkgkatltvdtssstaymqlssltsedsavyycarnrd 120
 Gaps
 1 MGWSCIILFLVSTATSVYSVOLQOPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 1 mgwsciilflvatatgvhsqvqlqqpgaelvkpgasvklsckasgytftsywmqwvkqrp 60
 New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
 ö
 Length 464;
 17; Indels
Kimihisa I;
 Reference Example 4; Page 187-188; 292pp; English.
 Score 615; DB 19;
Pred. No. 3.8e-43;
 Pred. No. 3.8e
5; Mismatches
 Mouse anti-Fas antibody HFE7A heavy chain.
Jun O, 1
Hideyuki H, Hiroko Y, J
O, Nobufusa S, Shin Y,
 B14747 standard; Protein; 464 AA.
 :: | || ||:|||||
121 ysnnwyfdvwgtgttvtvss 140
 121 DGWDYAIDYWGQGTSVTVSS 140
 Query Match 81.2%;
Best Local Similarity 84.3%;
Matches 118; Conservative
 (first entry)
 WPI; 1998-543440/47.
 464 AA;
 N-PSDB; V71029
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs. (Complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allower longing graft rejection. The present sequence represents the heavy chain of the murine anti-human Fas monoclonal antibody HFETA,
 Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; derit-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosupressive, thyrominetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HEFA; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 eventive or treating agent for the diseases caused by an abnormality the Fas/Fas ligand system e.g. autoimmune diseases, contains
 61 GOGLEWIGEIDPSESNINYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
 ö
 Score 615; DB 21; Length 464;
Pred. No. 3.8e-43;
5; Mismatches 17; Indels
 17; Indels
 Murine anti-Fas antibody HFE7A heavy chain protein.
 Example 4; Page 67-68; 139pp; Japanese.
 W90897 standard; Protein; 464 AA
 5;
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 ysnnwyfdvwgtgttvtvss 140
 81.2%;
 99JP-0278301
 98JP-0276883
 84.38;
 08-AUG-2000 (first entry)
 Best Local Similarity 84.3
Matches 118; Conservative
 Preventive or treating
 (SANY) SANKYO CO LTD.
 WPI; 2000-485645/43.
 464 AA;
 anti-Fas antibody
 N-PSDB; A72108.
JP2000169393-A.
 30-SEP-1999;
 30-SEP-1998;
 20-JUN-2000
 Sequence
 Query Match
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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

C molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

C apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,
anti-memic, antidiabetic, anti-alergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyronimetic,
antirheumatic, nephrotropic, antimifertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cells surface Fas or inhibit it by competitive
c inhibition of ligand binding. (I) are used to treat and/or prevent
cinhibition of ligand binding. (I) are used to treat and/or prevent
c inhibition of services. The standard system, especially systemic
c inhibition of services. Siorgen's syndrome, pernicious or hypoplastic
cupus erythematosus, Hashimnoto disease, rheumatoid arthritis, graft
versus host disease, Slorgen's syndrome, pernicious or hypoplastic
c anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
c disease, autodimmune hemolytic anemia, sterility, myasthenia gravis,
c multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
c dependent diabetes mellitus, alleray, arteriosclerosis, myocarditis,
c ardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
c (B, C or D) or alcoholic), and transplant rejection;
c multiple apoptosis in normal cells but selectively induce it in abnormal
c (B, C or D) or alcoholic), and transplant rejectively induce it in abnormal
c murine disease models. (I) act on the active site of Fas, ie. they mimic
c the native ligand, do not induce liver disease, and have reduced risk of
murine anti-relamentine anti-body response. This sequence represents
a murine anti-relamentine
c multiple and prevention
 ö
 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
 Gaps
 9
insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
 ;
 Nakahara K, Tamaki I, Takahashi T;
 Length 464;
 Indels
 Example reference 4; Page 100-102; 263pp; English.
 Query Match 81.2%; Score 615; DB 21;
Best Local Similarity 84.3%; Pred. No. 3.8e-43;
Matches 118; Conservative 5; Mismatches 17;
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 ysnnwyfdvwgtgttvtvss 140
 99EP-0307711.
 98JP-0276881
 98JP-0276882
 Serizawa N, Haruyama H,
 method of the invention.
 (SANY) SANKYO CO LTD.
 WPI; 2000-258930/23.
N-PSDB; A11546.
 464 AA;
 Mus musculus.
 30-SEP-1998;
 29-SEP-1999;
 30-SEP-1998;
 05-APR-2000.
 EP990663-A2
 Sequence
 qq
 à
 g
 qq
 ð
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121 ygyddamdywgggtsvtvss 140

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Peptide
 Protein
 W24025;
 Domain
 Domain
 Region
 Region
 Region
 Region
 Key
 W24025
 ö
 GOGLEWI 3EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIIJFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Gaps
 MAD 55.1 (EC.CC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min humanised 55.1 constructs have been expressed in myeloma
 Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monocional artibody; MAD; immunotherapy; therapy; diagnosis; transgenic arimal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
 Antigen bind..ng structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
 .
0
 Paterson DS;
 20..464
/label= Mat_protein
/note= "claim 3, page 97-98"
 Hall SM,
 1..19
/label= Sig_peptide
 Location/Qualifiers
 Disclosure; 'ig.15; 121pp; English.
 R76088 standard; Protein; 464 AA.
 Copley CG,
 121 DGWDYAIDYWGQGTSVTVSS 140
 94GB-0011089.
93GB-0024819.
 94WO-GB02610
 Query Match
Best Local Similarity 80.0%
Matches 112; Conservative
 (first entry)
), Boot C,
Wright AF;
 MAb 55.1 heavy chain.
 WPI; 1995-215262/28.
 (ZENE) ZENECA LTD.
 cells and E. coli.
 4 54 AA;
 N-PSDB; Q94037.
 29-NOV-1994;
 03-JUN-1994;
 03-DEC-1993;
 21-NOV-1995
 WO9515382-A
 08-JUN-1995
 Д,
 Sequence
 Rose MS,
 Peptide
 Protein
 R76088;
 Mus sp.
 Blakey
 61
 Key
RESULT
R76088
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This sequence represents a novel single chain antigen hybrid receptor (HR) and contains an extracellular domain specific for the hapten 4-hydroxy-5-iodo-3-nitrophenyl accetate (NRP) coupled to the CD8-alpha region and the transmembrane and signal-conducting intracellular parts of the CD3-zeta molecule. Such hybrid receptors comprise a receptor part olcalised on the outside of the cell and specific to a particular signal molecule and a receptor part originating from another receptor, localised on the inside of the cell and capable of setting off a signal inside the cell. The cell should also contain at least one other gene construct with a control region which can interact with the signal sent out by the hybrid receptor and thereby control expression of a transgene bound to this control region. Such cells are useful in gene therapy or for
 /label= VL_B_1-8
/note= "variable light chain region of B1-8 antibody"
 /label= VH_B_1-8
/note= "variable heavy chain region of B1-8 antibody"
 Cells with hybrid receptor having extracellular and intracellular regions of different origins – useful in gene therapy and diagnosis
 Hybrid receptor; single chain antigen; gene therapy; diagnosis; signal conduction; receptor; control region.
 "single chain antigen hybrid receptor"
 (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
 transmembrane_domain
 /label= cytoplasmic_domain
 Rosenthal F;
 CD_8-alpha_hinge
 1. 19
//abel= leader_peptide
 /label= (Gly,_Ser)3
/note= "linker region"
 Single chain antigen hybrid receptor.
 Location/Qualifiers
W24025 standard; Protein; 443 AA.
 Example 3; Fig 4; 46pp; German.
 Mertelsmann R,
 95DE-4045351
 96WO-DE02334
 (first entry)
 .330
 ..444
 140..154
 . 264
 265..309
 ..139
 /label=
 /label=
 /note=
 WPI; 1997-319784/29.
 N-PSDB; T77137
 WO9720938-A2.
 Homo sapiens.
 Kulmburg P,
 03-DEC-1996;
 05-DEC-1995;
 12-JUN-1997
 04-MAR-1998
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 Synthetic
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RESULT
 P70624
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 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Gaps
 .09
 9
 Monoclonal antibody; complementarity determining region; framework; antigens; tumour; melanoma; carcinoma; glioma; light; heavy; variable; chain.
 The variable heavy chain of monoclonal antibody 425 was prepd. from a synthetic cDNA sequence in which mutations had been made to the 5' and 3' ends to allow for cloning into HCMV expression vectors.
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP
 1;
 Human monoclonal antibodies binding to human receptors - for treatment and diagnosis of tumours, e.g. melanoma and carcinoma
 Length 443;
 Indels
 DB 18;
 20:
 Score 594.5; DB 1
Pred. No. 1.7e-41;
 6; Mismatches
 /nocc
20..140
/note= "mature protein"
 Saldanha
 'note= "signal peptide"
 Location/Qualifiers
 Š
 VH425 antibody cloned into pUC18.
 Disclosure; Fig 2; 89pp; English.
 R27049 standard; Protein; 140
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 ygssy-fdywgqgttvtvss 139
 69..85
/label- CDR2
118..129
/label- CDR3
 Kettleborough CA,
 78.5%;
80.7%;
 50..54
/label- CDR1
 92WO-EP00480
 91EP-0103389
 (first entry)
 (MERE) MERCK PATENT GMBH.
 Best Local Similarity 80.7
Matches 113; Conservative
 diagnostic purposes
 WPI; 1992-331729/40.
N-PSDB; Q28739.
 443 AA;
 01-MAR-1993
 04-MAR-1992;
 06-MAR-1991;
 WO9215683-A.
 17-SEP-1992.
 Bendlg MM,
 Synthetic
 Sequence
 Query Match
 Key
Peptide
 Protein
 R27049;
 Region
 Region
 Region
 RESULT
R27049
SXS
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61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Gaps
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 The patentors claim a chimeric antibody molecule comprising 2 light chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonuclectides (UIGs) for use as primers or probes for cloning immunoglobulinlight or heavy chain manns or genes. Depending on the nature of design of a particular UIG, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific J sequence. UIG denotes universal immunoglobulin gene.
 Sequence encoded by anti-hepatitis B heavy chain variable region in pING2006E.
to
 recombinant
 ő
 to cancer
Donor splice sites were recreated in the 3' flanking regions tallow correct splicing of the variable and constant regions. 5' sequence was altered to introduce an initiation codon. The cloned antibody may be used int the prodn.of reshaped or humanised antibodies which are less immunogenic than native antibodies and may be used to combat e.g. glioma, melanoma or carcinoma.
 Length 140;
 Score 589; DB 13; Length 14
Pred. No. 1.5e-41;
6; Mismatches 21; Indels
 - 1s by r
 Prodn. of immunoglobulin chains and molecules DNA procedures, with chimeric antibodies etc. specific antigens.
 ä
 Wall
 Chimeric antibody; Anti-cancer antibody
 Horwitz AH,
 ¥.
 Example; Fig 12B; 126pp; English.
 P70624 standard; protein; 136
 121 DGWDYAIDYWGQGTSVTVSS 140
 77.8%;
80.7%;
 86WO-US02269.
 85US-0793980.
 GENETIC ENG INC
 (first entry)
 Best Local Similarity 80.7
Matches 113, Conservative
 WPI; 1987-136004/19.
N-PSDB; N70967, N70968.
 Robinson RR, Liu AY,
 (ITGE-) INT GENETIC EN (ROBI/) ROBINSON R R.
 140 AA;
 27-0CT-1986;
 01-NOV-1985;
 09-APR-1991
 WO8702671-A.
 07-MAY-1987
 Seguence
 Query Match
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(XOMA) XOMA CORP
 Sequence
 Protein
 Peptide
 W16340;
 13
 Key
 RESULT
W16340
 Dp
5555555555
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 g
 δ
 g
 δy
 5
 61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCII), PLUSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Gaps
 The CDNA secuence encoding present anti-hepatitis B heavy chain variable secuence, was used in the preparation of a movel bolynucleotide molecule encoding an Ig fragment. The DNA molecule comprises 2 DNA sequences encoding 2 pectate lyase secretion signal sequences respectively linked to a DNA sequence from Ight chain, operably linked to a single prokeryotic promoter so as to form a dicistronic transcripticn unit, provided that the Ig fragment can bind an
 Immunoglobulin G; IgG; heavy chain; recombinant production; antibody; passive immunisation; serum sickness; anaphylactic shock; immunoassay; imaging; reagent; complement mediated lysis; therapy; hepatitis B virus; variable region; HBV.
 Nucleic acić encoding immunoglobulin fragment - comprising
di:cistronic transcription unit with pectate lyase signal sequences
 4,
 Length 136;
 Score 586; DB 8; Length 13:
Pred: No. 2.6e-41;
....matches 17; Indels
 Robinson RR;
 Anti-hepatitis B heavy chain variable region.
 5; Mismatches
 Liu AY,
 W10584 standard; Protein; 136 AA
 Example; Fig 12B; 95pp; English.
 Lei S,
 121 DGWDYAINYWGQGTSVTVSS 140
 90US-0501092.
85US-0793980.
86WO-US02269.
87US-0077528.
92US-0987555.
94US-0299085.
 Query Match
77.4%;
Best Local Simi.arity 81.4%;
Matches 114; Conservative
 85US-0793980
 (first entry)
 Better M, Horwitz AH,
Wall R, Wilcox GL;
 WPI; 1997-107579/10.
N-PSDB; T36303, T36304.
 (XOMA) XOMA CORP.
 AA;
 1:6
 11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
 01-NOV-1985;
 01-NOV-1985;
27-OCT-1986;
 21-OCT-1997
 US5595898-A.
 29-MAR-1990;
 21-JAN-1997
 987
 Sequence
 24-JUL-1
 Mus spp.
 W10584;
 RESULT 12
 XX
So
 qq
 g
 g
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Gaps
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Antibody engineering; heavy chain; light chain; chimaeric antibody; passive immunisation; diagnosis; hybridoma; hepatitis B virus; HBSAg; pING2006E; pING2012E.
antigen and is produced and secreted by an E. coli host cell when the nucleic acid molecule is expressed in the host cell.

The polynuclocided molecule is used for the production of recombinant antibodies; which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging reagents, in complement mediated lysis and for therapeutic purposes when coupled to a toxin or other therapeutic agent.
 4;
 Length 136;
 "mouse heavy chain variable region"
 17; Indels
 Mouse-human chimaeric anti-hepatitis B heavy chain.
 Score 586; DB 18;
Pred. No. 2.6e-41;
5; Mismatches 17;
 /note= "human J region"
117
 Location/Qualifiers
 Ą
 W16340 standard; Protein; 136
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 d-w---faywgggtlvtvss 136
 90US-0501092.
85US-0793980.
86WO-US02269.
 87US-0077528.
88US-0142039.
92US-0870404.
94US-0235225.
 77.4%;
81.4%;
 85US-0793980
 /label= VH
 (first entry)
 Query Match 77.49
Best Local Similarity 81.49
Matches 114; Conservative
 115..117
 Chimaeric Mus sp.;
Chimaeric Homo sapiens.
 /note=
 136 AA;
 Misc-difference
 01-NOV-1985;
 11-JAN-1988;
17-APR-1992;
29-APR-1994;
 04-SEP-1997
 01-NOV-1985;
27-OCT-1986;
 US5618920-A.
 08-APR-1997
 29-MAR-1990
 24-JUL-1987
```

us-08-700-737-15.rag

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94US-0357234
 Query Match
Best Local Similarity
Matches 114; Conserv
 Lei S,
 136 AA;
 (XOMA) XOMA CORP.
 09-DEC-1994;
 Homo sapiens
 05-JUN-1998
 USS698435-A.
 Better M,
 Sequence
 RESULT 15
 W47510
 QQ
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 q
 à
 ä
 Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin; protein production; human; constant region; passive immunisation; toxin; serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm; antlbody; Ig; heavy-chain; hepatitis; mouse; chimera.
 61 GOGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Gaps
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 A chimaeric polypeptide (W16340) comprises a mouse anti-HBsAg heavy chain variable region (derived from hybridoma ATCC CRL8017) and a human J region sequence. It is encoded by DNA sequences in plasmids pINC2006E (T70857) or pINC2012E (T70858). A complete polypeptide, comprising the mouse anti-HBsAg heavy chain variable region and human constant region, has been expressed in bacterial and transfected mouse cell hosts. Gene amplification has allowed prodn. of chimaeric heavy chain.
 Secretable immunoglobulin heavy and light chain fragments - capable of assembling into chimeric antibodies, useful for e.g. passive immunisation, diagnosis, etc
 4;
 Length 136;
 17; Indels
 Liu AY, Robinson RR;
 Chimeric anti-hepatitis heavy chain from pING2006E.
 Score 586; DB 18;
Pred. No. 2.6e-41;
5; Mismatches 17;
 Example 2; Fig 12B; 96pp; English.
 W10239 standard; Protein; 136 AA.
 'n
 Lei S,
 121 DGWDYAIDYWGQGTSVTVSS 140
 77.48;
81.48;
 85US-0793980.
86WO-US02269.
87US-0077528.
 88US-0142039.
92US-0987555.
93US-0020671.
 85US-0793980
 90US-0501092
 05-AUG-1997 (first entry)
 Matches 114; Conservative
 Chimeric - Homo sapiens.
Chimeric - Mus musculus.
 Horwitz AH, Wilcox GL;
 WPI; 1997-225473/20.
N-PSDB; T70857-58.
 Best Local Similarity
 Sequence 136 AA;
 27-0CT-1986;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
22-FEB-1993;
 01-NOV-1985;
 US5576195-A.
 29-MAR-1990;
01-NOV-1985;
 19-NOV-1996
 Better M,
Wall R,
 Query Match
 W10239;
 RESULT 14
 121
 W10239
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This sequence represents a fragment of the human-mouse chimeric anti-hepatitis heavy chain encoded by the gene contained within processors. PinG2006E. WinG2006E. PinG2006E was used in the method of the invention to express the chimeric heavy chain. The method of the invention to express the chimeric heavy chain. The method of the invention of a protein in a Gram-negative bacterium. The method improves on current techniques, by using a vector including DNA encoding the pectate lyase signal sequence (see T51034), attached to the sequence encoding the protein for production. The method is especially used to make immunoglobulins (Ig), particularly those with a human constant region, suitable for passive immunosation (without risk of serum sickness or anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The ignay also be used therapeutically, optionally coupled to toxins, etc.

Alternatively the protein to be produced is the sweetener thaumatin. The presence of this signal sequence means that the protein is exported from the cytoplasm and can be recovered from the culture medium or periplasm, and can be recovered from the culture medium or periplasm, and can be except human-human ig are of M class, easily creduced and aggregated, and these can now be changed to G, A or E
 61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 sequence - from pectate lyase to ensure transport of protein from the cytoplasm, esp. for prodn. of antibodies
 Improved prodn. of protein in Gram -ve bacteria using signal sequence - from pectate lyase to ensure transport of protein
 Length 136;
 Mouse; murine; human anti-hepatitis antibody; heavy chain; immunoglobulin fragment production; Iq fragment production; monoclonal antibody L6; human lung carcinoma cell.
 77.4%; Score 586; DB 18;
81.4%; Pred. No. 2.6e-41;
ive 5; Mismatches 17;
Wilcox GL;
 Human anti-hepatitis antibody heavy chain.
 Example 2; Fig 12B; 86pp; English.
 W47510 standard; Protein; 136 AA
Robinson RR,
 121 DGWDYAIDYWGQGTSVTVSS 140
 (first entry)
 Conservative
 WPI; 1997-011254/01.
N-PSDB; T51039.
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Job time: 119 sec

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The present sequence was used in the development of a novel method-
for the production of an immunoglobulin (Ig) fragment capable of
binding an antigen. The method comprises culturing an E. Coli host
that has been transformed with a nucleic acid molecule encoding the
influence of the nucleic acid molecule comprises DNA sequences
encoding: (a) pectate lyase secretion signal sequence
influence of DNA sequence encoding at least the variable region of
influence of the influence of the comprises of the variable region of an Ig light chain, where (a) and (b) are operably linked
to a single profazior promoter to form a dicistronic
cranscription unit. The method is used to produce chimeric Fab
molecules, e.g. derived from murine monoclonal antibody L6 raised
against human lung carcinoma cells. The invention provides a novel
approach for producing genetically engineered antibodies of
desired variable region specificity and constant region
ceptical gene synthesis, recombinant DNA cloning and production of
specific Ig chains in various organisms. The application of
chemical gene synthesis, recombinant DNA cloning and production of
solution for the efficient large scale production of human
monoclonal antibodies. The invention also provides a solution to
the problem of class switching antibody molecules.
 {\tt DNA} encoding secretable immunoglobulin fragments - comprising at least the variable regions of light or heavy chains
 Robinson RR;
 Liu AY,
 Example II; Fig 12B; 98pp; English.
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 95US-0467140
 90US-0501092
85US-0793980
 86WO-US02269
 87US-0077528
88US-0142039
 92US-0987555
94US-0299085
 95US-0467140
 WPI; 1998-051492/05.
N-PSDB; V18553, V18554.
 Better M, Horwitz AH, Wall R, Wilsox GL;
 (XOMA) XOMA CORP.
 06-JUN-1995;
 29-MAR-1990;
01-NOV-1985;
 08-DEC-1992;
 06-JUN-1995
16-DEC-1997
 27-0CT-1986
 11-JAN-1988
 18-AUG-1994
 24-JUL-1987
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Search completed: April 13, 2001, 15:35:40

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

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 Seguence 78,
 Sequence Seq
 APPLICANT: Foncith, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Nomes, S. Tarran
APPLICANT: Johnson, Soldanha, Jos
APPLICANT: Saldanha, Jos
APPLICANT: Baldanha, Jos
APPLICANT: Baldanha, Jos
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
FOREX/AGREET.
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7 US-09-322-662-26

0 US-09-608-705-11

1 US-08-700-737-55

8 US-09-408-646-145

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8 US-09-408-662-147

8 US-09-408-662-147

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US-08-073-967-44
US-08-553-497-12
US-08-286-754-78
 US-09-753-436-78
 ALIGNMENTS
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
 ; Sequence 15, Application US/08700737 ; GENERAL INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 ADDRESSEE: Hamilton, E
STREET: Two Militia Dr
CITY: Lexington
STATE: Massachusetts
 USA
 02173
 US-08-700-737-15
 544.5
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Sequence 4, Appli
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Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 24, Appli
Sequence 24, Appli
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US-08-700-737-9

US-08-700-737-9

US-08-700-737-19

US-09-053-583-9

1 US-09-053-583-9

1 US-09-0648-646-9

1 US-09-499-662-9

US-08-497-165-24

US-08-692-084-26
 Total number of hits satisfying chosen parameters:
 1009251 seqs, 160854530 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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 Length
 Query
Match
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Score

Result Š

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 Massachusetts
 CORRESPONDENCE ADDRESS:
 ; TOPOLOGY: linear
US-08-700-737-2
 Best_Local Similarity
Matches 135; Conserv
 STRANDEDNESS:
 02173
 ADDRESSEE:
 COUNTRY:
 Query Match
 67
 RESULT
 Db
 ÖŻ
 qq
 ŏ
 61 GQGLEWI(EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 61 GQGLEWI(.EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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 APPLICANT: Sendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
 Length 140;
 Indels
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington CITY: ASARTE: Massachusetts
 PatentIn Release #1.0, Version #1.30
 Score 757; DB 11;
Pred. No. 4.4e-65;
Mismatches 0;
 ATTORNEY AGE NT INFORMATION:
NAME: Brock, David E.
RECISTRATION NUMBER: 22,592
REFERENCE, DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
 COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
 Sequence 4, App.ication US/08700737 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (517) 861-540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
 100.0%; Sc
100.0%; Pr
tive 0;
 APPLICANT: Condth, Paul D.
APPLICANT: Condth, Paul D.
APPLICANT: Condes, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
 TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 DGWDYAII)YWGQGTSVTVSS 140
 SEQUENCE CHIRACTERISTICS:
 Matches 140; Conservative
 ; MOWLECULE TYNE: protein US-08-700-737-4
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
 MOLECULE TYPE: protein US-08-700-737-15
 NUMBER OF SEQUENCES:
 linear
 Query Match
Best Local Similarity
 CLASSIFICATION:
 JSA
 TOPOLOGY:
 SOFTWARE:
 TOPOLOGY:
 COUNTRY:
 US-08-700-737-4
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0;
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 IGEIDPSESNINVNOKFKGKATLTVDISSSTAYMOLSSLTSEDSAVYCARGGYDGWDYA 126
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 1 MGWSCIILFLYSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 APPLICANT: Noneth, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Singler, Douglas J.
APPLICANT: Saldanha, Jos
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF SEQUENCES: 63
 ;
0
 0;
 Length 144;
Length 137;
 1; Indels
 Indels
 Hamilton, Brook, Smith & Reynolds, P.C.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC COMPUTIONS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 94.2%; Score 713; DB 11;
99.3%; Pred. No. 7.7e-61;
:ive 0; Mismatches 1;
Score 730; DB 11;
Pred. No. 1.7e-62;
0; Mismatches 2;
 ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
 APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
 US-08-700-737-2; Sequence 2, Application US/08700737; GENERAL INFORMATION:
 STREET: Two Militia Drive CITY: Lexington
 96.4%;
98.5%;
 TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
 Query Match 94.2%
Best Local Similarity 99.3%
Matches 133; Conservative
 121 DGWDYAIDYWGQGTSVT 137
 DGWDYAIDYWGQGTSVT 137
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TITLE OF INVENTION: Anti-Fas Antibodies FILE REFERENCE: 980126/HG
 RESULT 6
US-09-053-583-9
Sequence 9, Application US/09053583A;
GENERAL INFORMATION:
APPLICANT: SCRIZAWA, Nobufusa;
APPLICANT: ICHIKAWA, KIMIHISA
 FILING DATE: 15-40G-1996
CLASSIFICATION: 435
ATORNEY-AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-640
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
 APPLICANT: Ohsumi, Jun
APPLICANT: Ohsumi, Jun
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Tohru
APPLICANT: Shiraishi, Akio
APPLICANT: Yonehara, Shin
 83.9%;
86.7%;
 Best Local Similarity 86.7
Matches 117; Conservative
 126 AIDYWGQGTSVTVSS 140
 126 AIDYWGQGTLVTVSS 140
 ; MOLECULE TYPE: protein US-08-700-737-19
 Query Match
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67 IGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYA 126
 80 NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWGQGTSVTVS 139
 20 QVQLQQPGAELVKPGTSVKLSCKGYGFTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
 APPLICANT: Ringler, Douglas J.
APPLICANT: Numan, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bandanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH 4 7
TITLE OF INVENTION: HUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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 Query Match 86.9%; Score 658; DB 11; Length 121; Best Local Similarity 100.0%; Pred. No. 1.2e-55; Matches 121; Conservative 0; Mismatches 0; Indels
 COUNTY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIPICATION: 4355
 Sequence 9, Application US/08700737 GENERAL INFORMATION:
 ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTATION NUMBER: 22,592
REFERENCE/DOCKET UNMBER: LKS9:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 9:
 Sequence 19, Application US/08700737 GENERAL INFORMATION:
 APPLICANT: Ponath, Paul D.
 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
 127 IDYWGQGTSVTVSS 140
 127 IDYWGQGTSVTVSS 140
 CITY: Lexington
STATE: Massachusetts
 ; TOPOLOGY: linear
US-08-700-737-9
 US-08-700-737-9
 US-08-700-737-19
 140 S 140
 121 $ 121
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 APPLICANT: Ringler, Douglas J.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Saldanha, Jos
APPLICANT: Baldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HURANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
CITY: Lexington
CITY: Lexington
STARE: Massachusetts
COUNTY: USA
 Length 180;
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 COUNTRY:
ZIP: 02173
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
TITING DATE: 15-AUG-1996
 Score 635; DB 11;
Pred. No. 3.1e-53;
8; Mismatches 10;
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 17;
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Pred. No. 7.8e-51;
 Score 615; DB 14;
Pred. No. 7.8e-51;
 APPLICANT: Serizava, Nobufusa APPLICANT: Serizava, Hideyuki APPLICANT: Hariyama, Hideyuki APPLICANT: Hariyama, Hideyuki APPLICANT: Tamaki, Ikuko APPLICANT: Tamaki, Ikuko TITIE OF INVENTION: ANTI-Fas Antibodies TITIE REFERENCE: 990540/HG CURRENT APPLICATION NUMBER: US/09/408,646A CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION UNMBER: JP 10-276881
EARLIER PILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 165
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EARLIER APPLICATION NUMBER: JP HEI 9-82953
EARLIER FILING DATE: 1997-04-01
EARLIER FILING DATE: 1997-06-25
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EARLIER FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 123
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US/09/053,583A
 Sequence 9, Application US/09408646A GENERAL INFORMATION:
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 US-09-408-646-9
 LENGTH: 464
 TYPE: PRT
 SEQ ID NO 9
 TYPE: PRT
 SEG ID NO 9
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 Indels
 Sequence 24, Application US/08487165
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Retileborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
WUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
 3: Millen, White, Zelano & Branigan, P.C. 2200 Clarendon Boulevard, Suite 1400
 SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,165 FILING DATE: 07-JUN-1995 PRIOR APPLICATION DATA: RAPLICATION DATA: US 07/946,421 FILING DATE: 06-NOV-1992
 Score 615; DB 18;
Pred. No. 7.8e-51;
5; Mismatches 17;
Sequence 9, Application US/09499662
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Hakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
TITLE REPRENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/09/499,662
CURRENT APPLICATION NUMBER: US 09/053,583
EARLIER PPLICATION NUMBER: US 09/053,583
EARLIER PILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 9
LENGTH: 464
 PC-DOS/MS-DOS
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 YSNNWYFDVWGTGTTVTVSS 140
 Query Match 81.2%;
Best Local Similarity 84.3%;
Matches 118; Conservative
 COMPUTER READABLE FORM:
 ; ORGANISM: Mus musculus US-09-499-662-9
 CITY: Arlington STATE: Virginia
 COUNTRY: U.S.A.
 ADDRESSEE:
STREET: 22
 RESULT 9
US-08-487-165-24
 TYPE: PRT
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 Sequence 26, Application US/08779784
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
 ö
 Length 143;
 23; Indels
 ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 70S/08/779,784
 Score 583; DB 10;
Pred. No. 2.4e-48;
5; Mismatches 23;
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 FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
REGISTRATION NUMBER: 26,742
 Z1F: 0.00.4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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 121 YYGSRNFDYWGQGTTLTVSS 140
 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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80.0%;
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amino acid
 Query Match 77.0
Best Local Similarity 80.0
Matches 112; Conservative
 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
US-08-692-084-26
 protein
 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 linear
 MOLECULE TYPE:
 ZIP: 07601
 RESULT 11
US-08-779-784-26
 TOPOLOGY:
 US-08-779-784-26
 q
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 ò
 US-08-692-084-26
Sequence 26, Application US/08692084
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Asakura, Kunihiko
TILE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION USING MONOC
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STRRET: 411 Hackensack Ave, Continental Plaza, 4th
STRRET: Floor
 ö
 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 61 GOGLEWIGEFNPSNGRINYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASRDY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Length 140;
 Score 589; DB 8;
Pred. No. 6.2e-49;
6; Mismatches 21.
 REFERENCE/DOCKET NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEPHONE: 703-243-6410
TELER: 64191
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 140
 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIP
 APPLICATION NUMBER: US/08/692,084
FILING DATE: 08-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-ARR-1994
ATTORNEY/AGENT INFORMATION:
EP 911933892
 Patentin Release #1.0,
 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
 121 DYDGRYFDYWGQGTTLTVSS 140
 121 DGWDYAIDYWGQGTSVTVSS 140
 Query Match 77.8%;
Best Local Similarity 80.7%;
 FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
 NAME: Hamlet-King, Diana REGISTRATION NUMBER: 33,
 Floppy disk
 LENGTH: 140 amino acids TYPE: amino acid
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
 Matches 113; Conservative
 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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 07603
 ; TOPOLOGY:
US-08-487-165-24
 COUNTRY:
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TOPOLOGY:
 Query Match
 LENGTH:
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 DIAGNOSTIC AND THERAPEUTIC
IN THE CENTRAL NERVOUS SYSTEM
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 61 GGGLEWI;NINPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYARRAP 120
 61 GQGLEWIG NINPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYYARRAP 120
 61 GQGLEWI; EIDPSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCII.JFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 1 MGWSCIIIFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Gaps
 APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Kospen, H.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of FILE BEPERENCE: P1777R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT APPLICATION NUMBER: 2000-10-27
 ..
0
 0
 Length 143;
 Length 143;
 Indels
 23; Indels
 Score 583; DB 17;
Pred. No. 2.4e-48;
Score 583; DB 11;
Pred. No. 2.4e-48;
5; Mismatches 23;
 APPLICANT: Rorriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pesse, Larry R.
ITLLE OF INVENTION: HUMAN IGM ANTIBODIES, AND ITILE OF INVENTION: USBS THEREOF PARTICULARLY FILE REFERENCE: 1199-1-005
 5; Mismatches
 CURRENT APPLIC! TION NUMBER: US/09/322,862
CURRENT FILING DATE: 1999-05-28
 JMBER: 08/779,784
1997-01-07
 PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
 Sequence 11, Application US/09698705 GENERAL INFORMATION:
 Sequence 26, Aprlication US/09322862 GENERAL INFORMATION:
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 YYGSRNF DYWGOGTTLTVSS 140
 DGWDYAII YWGQGTSVTVSS 140
 121 YYGSRNFI YWGOGTTLTVSS 140
 77.0%;
 Query Match 77.0%;
Best Local Similarity 80.0%;
Matches 112; Conservative
 Conservative
 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-0
 ; ORGANISM: Mus musculus
US-09-322-862-26
 Query Match
Best Local Simi.arity
Matches 112; Conserv
 RESULT 12
US-09-322-862-26
 US-09-698-705-11
 SEQ ID NO 26
LENGTH: 143
 APPLICANT:
APPLICANT:
 121
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 61 GRGLEWIGRIDPSDSEIHYDQKFKDKATLTVDKSSSTAXIQLSSLTSEDSAVYXCALTGI 120
 9
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Gaps
 TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7 TITLE OF INVENTION: INTEGRIN NUMBER OF SEQUENCES: 63
 4;
 Length 466;
 Indels
 Brook, Smith & Reynolds, P.C
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
 ; OTHER INFORMATION: sequence is chimeric mouse/human US-09-698-705-11
 76.9%; Score 582; DB 20;
ilarity 79.3%; Pred. No. 1.2e-47;
Conservative 11; Mismatches 14;
 us 60/162,558
 US-08-700-737-55; Sequence 55, Application US/08700737; GENERAL INFORMATION:
 APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
 ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/POCKET NUMBER: LKA
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 ----YAMAYWGQGTSVTVSS 136
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 11
 Two Militia Drive
 TYPE: PRT ORGANISM: Artificial sequence
 TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
 Massachusetts
 CORRESPONDENCE ADDRESS:
 Best Local Similarity
Matches 111; Conserv
 Lexington
 FILING DATE: 15 CLASSIFICATION:
 STRANDEDNESS
 02173
 ADDRESSEE:
 STREET:
 COUNTRY:
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us-08-700-737-55

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ó;
 Gaps
 20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
 1 QVQLVQSGAEVKKPGASVKVSCKGSGYTFTSVWMHWVRQAPGQRLEWIGEIDPSESNTNY 60
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-09-408-646-143
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 75.6%; Score 572; DB 11; Length 121; 86.0%; Pred. No. 2.2e-47; 1.ve 7; Mismatches 10; Indels
 Sequence 143, Application US/09408646A
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamani, Ikuko
APPLICANT: Tamani, Ikuko
APPLICANT: Tamani, Ikuko
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 990540/HG
CURRENT APPLICATION NUMBER: US/09/408,646A
CURRENT FILING DATE: 1999-09-30
BARLIER APPLICATION NUMBER: JP 10-276881
BARLIER FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 165
SEQ ID NOS: 165
LENGTH: 470
Query Match
Best Local Similarity 86.0%
Matches 104; Conservative
 RESULT 15
US-09-408-646-143
 140 S 140
 121 S 121
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1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60

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Query Match 74.9%; Score 567; DB 18; Length 470; Best Local Similarity 77.1%; Pred. No. 3.3e-46; Matches 108; Conservative 10; Mismatches 22; Indels

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Gaps

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121 DGWDYAIDYWGQGTSVTVSS 140 ô

121 YSNNWYFDVWGQGTLVTVSS 140

Search completed: April 13, 2001, 17:37:49 Job time: 166 sec

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April 13, 2001, 17:37:56 ; Search time 4.45 Seconds (without alignments) 54.611 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 OM protein - protein search,
 Perfect score:
 Scoring table:
 Sequence:
 Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

7695 seqs, 1735856 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending\_Patents\_AA\_New:\*

': /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*

': /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*

': /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

': /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

': /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

': /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\* . . . . . . Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                | Sequence 11, Appl Sequence 2, Appl Sequence 1, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 6, Appl Sequence 6, Appl Sequence 1334, Ap Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 6, Appl Sequence 8, Appl S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SUMMARIES                  | US-08-475-815A-11 US-09-386-658-2 US-09-386-658-2 US-09-509-031-16 US-09-509-031-11 US-09-509-031-11 US-09-509-031-6 US-09-509-031-6 US-09-509-031-6 US-09-739-449-12328 US-09-739-449-11638 US-09-739-449-11638 US-09-739-449-11638 US-09-739-449-11638 US-09-739-449-11638 US-09-739-449-11638 US-09-739-449-11639 US-09-739-449-11233 US-09-739-449-11233 US-09-815-108-6 US-09-815-108-6 US-09-815-108-6 US-09-815-108-6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| DB                         | • ፈለላ የመመመመመ መመመመመመመመመመመመመመመመመመመመመመመመመመመመመመ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| %<br>Query<br>Match Length | 2000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000 |
| %<br>Query<br>Match        | 2010<br>2010<br>2010<br>2010<br>2010<br>2010<br>2010<br>2010                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Score                      | 28 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Result<br>No.              | 12222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

| Sequence 15, Appl | Sequence 17, Appl | Sequence 19, Appl | Sequence 3. Appli | 2               | 2                | Sequence 10479. A   |                     | Sectionica 12808    | Section 26 April |                    | Sequence 302, Ap |                 | Sequence 10936 a    |                   |                     |                   | Sequence 12644, A   |
|-------------------|-------------------|-------------------|-------------------|-----------------|------------------|---------------------|---------------------|---------------------|------------------|--------------------|------------------|-----------------|---------------------|-------------------|---------------------|-------------------|---------------------|
| US-09-815-108-15  | US-03-815-108-17  | US-09-815-108-19  | US-09-815-108-3   | US-09-815-108-2 | US-09-815-108-22 | US-09-739-449-10479 | US-09-739-449-10300 | US-09-739-449-12898 | US-09-810-264-26 | US-09-739-449-8302 | US-09-813-742-5  | US-09-813-742-3 | US-09-739-449-10936 | US-09-809-391-481 | US-09-739-449-11627 | US-09-809-391-754 | US-09-739-449-12644 |
| 04 5              |                   | υ.                | 9                 | 29 5            | 94 5             | 18 5                | 12 5                | 51 5                | 72 5             | 22 5               | 52 5             | 14              | 15 5                | 71 5              | 58 5                | 11 5              | 91                  |
| 504               | ñi                | ก                 | ŭ                 | S               | Š                | 4                   | 11                  | 5                   | 1.               | č                  | 9                | 114             | 2                   | 5                 | 175                 | 1(                | 21                  |
| 7.7               |                   | · · ·             | 7.7               | 7.7             | 7.7              | 7.6                 | 7.6                 | 7.5                 | 7.5              | 7.5                | 7.4              | 7.4             | 7.3                 | 7.3               | 7.3                 | 7.3               | 7.3                 |
| 58.5              | 200               | 0.00              | 58.5              | 58.5            | 58.5             | 57.5                | 57.5                | 57                  | 56.5             | 56.5               | 99               | 26              | 55.5                | 55.5              | 55.5                | 55                | 55                  |
| 28                | N 6               | 2 4               | 1.                | 32              | 33               | 34                  | 35                  | 36                  | 37               | 38                 | 39               | 40              | 41                  | 42                | 43                  | 44                | 45                  |

## ALIGNMENTS

```
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Reff. Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LXMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
 STREET: 1100 New York Avenue, N.W., Ninth FL. CITY: Washington
 FILING DATE: 07-JUN-1995
CLASIPECATION:
PRIOR APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-00V-1993
PRIOR APPLICATION NUMBER: US 08/149,099
FILING DATE: 103-00V-1993
PRIOR APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-00V-1992
ATTOCNEY/AGENT INFORMATION:
NAME: TESKIn, ROBIN L.
 23522-0157
 Sequence 11, Application US/08475815A
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
 ADDRESSEE: PILLSBURY WINTHROP
 REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23:
TELECOMMUNICATION:
TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
 LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-815A-11
 USA
 STATE: DC
COUNTRY: US
ZIP: 20005
RESULT 1
US-08-475-815A-11
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RESULT 4
US-09-782-504-4
 149
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 qq
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0
 APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tratlinton, David M.
APPLICANT: Tratlinton, Herbert R.
AITLE OF INVENTOR: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PALGALIN Ver. 2.1
 61 GQGLEWI; JEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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 GQGLEWICEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
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 Gaps
 Gaps
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 Length 140;
 Indels
 24; Indels
 APPLICANT: Erlinger, Bernard
APPLICANT: Chen, Bi-Xing
TITLE OF INVENTION: ANTHRODIES SPECIFIC FOR FULLERENES
FILE REFERENCE: 0575-54182/JPM/SHS/NYM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT PILING DATE: 1999-08-31
 29;
 ; Score 549; DB 4;
; Pred. No. 9.1e-51;
10; Mismatches 24;
 DB 5;
 61.2%; Score 463; DB 5. 65.0%; Pred. No. 6e-42; ive 12; Mismatches
 Sequence 16, Application US/09509031 GENERAL INFORMATION:
APPLICANT: Koestgen, Frank
 Sequence 2, Application US/09386658 GENERAL INFORMATION:
 121 DGWDYAI JYWGQGTSVTVSS 140
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 121 YGGDWYFN VWGAGTTVTVSA 140
 DGWDYAILYWGQGTSVTVSS 140
 ORGANISM: Artificial Sequence
 NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
 Query Match 61.2%
Best Local Simi.arity 65.0%
Matches 91; Conservative
 Query Match 72.55
Best Local Similarity 75.77
Matches 106; Conservative
), ORGANISM: mouse [murine]
US-09-386-658-2
 US-09-509-031-16
 SEQ ID NO 16
LENGÎH: 482
 132
 US-09-386-658-2
 TYPE: PRT
 SEO ID NO 2
 LENGTH:
 120
 121
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2;
 TNYNQKFKGKATLITVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSV 136
 Gaps
OTHER INFORMATION: Description of Artificial Sequence:ccMTLgL protein corner in Propration: sequence US-09-509-031-16
 SQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESN 76
 |:|:| : | ||:|| |::|| |:||: ::| ||:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|
 8;
 Length 482;
 32.0%; Score 242; DB 5; Length 240; 47.9%; Pred. No. 6.4e-19; ive 24; Mismatches 31; Indels
 ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 Bruce, Kim Folger
Schreiber, George J.
Siegall, Clay
McAndrew, Stephen
TITLE OF INVENTION: ANTBODIES REACTIVE WITH HUMAN
CARCINOMAS
 DB 5;
 NAME: ROSENMAN Ph.D., Stephen J. REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 840065.405D3
 Score 282.5; DB Pred. No. 9.8e-23;
 27; Mismatches
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,504
FILING DATE: 12-Feb-2001
CLASSIFICATION: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-504-4
 Karl Erik
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
 Sequence 4, Application US/09782504
GENERAL INFORMATION
GENERAL HELISTOM, Ingegerd
Hellstrom, Karl Erik
 MEDIUM TYPE: Floppy disk
 LENGTH: 240 amino acids TYPE: amino acid
 37.3%;
 SEQUENCE CHARACTERISTICS
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS
 STATE: Washington
 Query Match 37.3%
Best Local Similarity 44.4%
Matches 55; Conservative
 INFORMATION FOR SEQ ID NO:
 Query Match 32.0
Best Local Similarity 47.9
Matches 58; Conservative
 NUMBER OF SEQUENCES:
 USA
 COUNTRY:
 137 TVSS 140
 TVSS 152
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us-08-700-737-15.rapn

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APPLICANT: Suess, dairiele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 342
 63 GLE-WIGEIDPSESNINYNQKFKGKATLIVDISSSTAY-MQLSSLTSEDSAVYYCARGGY 120
 64 SPKPWI--YATSNLASGVPVRFSGS------GSGTSYSLTISRVBAEDAATYYCQQ--- 111
 72 PSESNTNYNQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 130
 21 VOLQOPGAELVKPGTSVKLSCKG----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 71
 APPLICANT: SUSSES, GARGELE M.
APPLICANT: Tarlinton, David M.
APPLICANT: Traulinton, David M.
APPLICANT: Traulinton, David M.
TITLE OF INVENTION: CATALTIC ANTIBOIDES AND A METHOD OF PRODUCING SFILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
LENGTH: 155
 ; OTHER INFORMATION: Description of Artificial Sequence:TLHL protein; OTHER INFORMATION: sequence
US-09-509-031-6
 Length 155;
 Description of Artificial Sequence: Kappa protein sequence
 46; Indels
 14.1%; Score 107; DB 5; 27.3%; Pred. No. 3e-05; ive 19; Mismatches 46;
 ; Sequence 11, Application US/09509031
; GENERAL INFORMATION:
 Sequence 6, Application US/09509031; GENERAL INFORMATION: APPLICANT: Koentgen, Frank
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 121 DGWDYAIDYWGQGTSVTV 138
 --WTSNPPTFGGGTKLEI 127
 Query Match
Best Local Similarity 27.38
Matches 35; Conservative
 APPLICANT: Koentgen, Frank
 OTHER INFORMATION:
COTHER INFORMATION:
US-09-509-031-11
 134 GQGTKLEI 141
 131 GQGTSVTV 138
 US-09-509-031-11
 US-09-509-031-6
 FEATURE:
 FEATURE:
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 Sequence 7, Application US/08475815A
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Restetter, William H.
TITLE OF INVENTION: THERAPEDITE APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
 7;
 6 ILLFLVSTATSVHSQVQL---QQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQ 62
 20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY
 :||| : | ||:|| |:|:|| |:|:|| |:||:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:||
 Length 128;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A FILING DATE: 07-JUN-1995
DRICH APPLICATION:
 1100 New York Avenue, N.W., Ninth FL.
 Ouery Match 16.1%; Score 122; DB 4; Best Local Similarity 26.8%; Pred. No. 6.8e-07; Matches 37; Conservative 28; Mismatches 51
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
 23522-0157
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
 PILLSBURY WINTHROP
 NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 2352
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861.3000
TELEFAX: 202-822-0944
 TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
 LENGTH: 128 amino acids
 MOLECULE TYPE: protein US-08-475-815A-7
 Washington
 amino acid
 linear
 USA
 ADDRESSEE:
 TOPOLOGY:
 US-08-475-815A-7
 STATE: D
 140 S 140
 114 S 114
 STREET:
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RESULT 10
US-09-193-562D-28
 SEQ ID NO 28
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 US-09-739-449-9534
US-09-739-449-9534
US-09-739-449-9534
GENERAL INFORMATION:
Sequence 9534, Application US/09739449
GENERAL INFORMATION:
Storence 9534, Application US/09739449
GENERAL INFORMATION:
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REPERENCE: 38-10(14940)C
CURRENT APPLICATION NUMBER: US/09/739,449
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR PRICALING DATE: 2000-12-19
PRIOR FILING LATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
 7:
 APPLICANT: Suss, Gabriele M.
APPLICANT: Ta:linton, David M.
APPLICANT: Ta:linton, David M.
APPLICANT: Ta:linton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474 CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE REFERENCE: 13474 CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME FILE OF INTON NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SSC ID NO 4
LENGTH: 495
 72 PSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYAIDY-W 130
 72 PSESNIN; NQKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARGGYDGWDYAIDY-W 130
 32 VMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNY-LAWYQQKPGQPPKLLIYW---- 85
 21 VQLQQPGAELVKPGTSVKLSCKG----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 71
 Gaps
 21 VQLQQPG/ELVKPGTSVKLSCKG----YGYTFTSYWMHWVKQRPGQG----LEWIGEID 71
 32 VMTQSPD(:LAVSLGERATINCKSSQSVLYSSNSKNY-LAWYQQKPGQPPKLLIYW----
 28;
 ; OTHER INFORMATION: Description of Artificial Sequence:CATAB-TEV ; OTHER INFORMATION: protein sequence US-09-509-031-4
 28;
 14.1%; Score 107; DB 5; Length 495; 27.3%; Pred. No. 0.00011; tive 19; Mismatches 46; Indels
Length, 342;
 46; Indels
Query Match
Best Local Similarity 27.3%; Pred. No. 7.4e-05;
Matches 35; (onservative 19; Mismatches 46
 US-09-509-031-4; Sequence 4, App.ication US/09509031; GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 Conservative
 APPLICANT: Koentgen, Frank
 Local Similarity
nes 35; Conserv
 134 GQGTKLEI 141
 GQGTSVTV 138
 131 GQGTSVT" 138
 134 GQGTKLE: 141
 Query Match
 Best Loca
Matches
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NGS-09-732449-12328
| Sequence 12328, Application US/09739449
| Sequence 12328, Application US/09739449
| Sequence 12328, Application US/09739449
| GERRAL INFORMATION: Application of Sequences and USES Thereof TITLE OF INVENTION: Application of Sequences and USES Thereof TITLE OF INVENTION: Application NUMBER: US/09/739,449
| CURRENT APPLICATION NUMBER: US/09/739,449
| CURRENT FILING DATE: 2000-12-19
| PRIOR FILING DATE: 2000-02-23
 9
 -----QLSSLTSE---DSAVYYC---ARGGYDGW 123
 KA----DVKSLVWYVPENFEEAGYKVPESMEDLLKLTDQIVADGGTPWCIGLGSGGATGW 211
 65 EWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWD 124
 11 VSTATSVHSQ--VQLQQPGAELVKP----GTSVKLSCKGYGYTFTSYWMHWVKQRPGQGL 64
 28 AELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWI--GEIDPSESNTNYNQKFKG 85
 Sequence 28, Application US/09193562D
Sequence 28, Application US/09193562D
GEMERAL INFORMATION:
APPLICANT: Pauli, Benedicht U.
TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
FILE REPERENCE: 18617.0052
CURRENT APPLICATION NUMBER: US/09/193,562D
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US/60/065,922
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 47
 Length 914;
 Length 442;
 Indels
 8.8%; Score 66.5; DB 5; 25.0%; Pred. No. 3.4;
 5.
 ; Score 69.5; DB
; Pred. No. 0.72;
11; Mismatches
 17; Mismatches
 TYPE: PRT ORGANISM: Agrobacterium tumefaciens
; LENGTH: 442
TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9534
 NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 12328
LENGTH: 517
 9.2%;
25.0%;
 86 KATLTVDISSSTAYM-----
 Query Match
Best Local Similarity 25.0%
Matches 30; Conservative
 Query Match 8.8%
Best Local Similarity 25.0%
Matches 34; Conservative
 125 YAIDYWGQGTSVTVSS 140
 ; ORGANISM: Homo sapiens US-09-193-562D-28
```

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Sequence 4, Application US/09814950

GENERAL INFORMATION:
APPLICAMTON:
APPLICAMTON:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01174
CURRENT APPLICATION NUMBER: US/09/814,950
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FESTERE for Windows Version 4.0
 43 GYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQL 102
 90 GVGYQFNNYF-----RSDVTLDYMGKSDFRGSTSGFCGSVPGRC-VSADLSSLSAYTLM 142
 19 SQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTN 78
 :: |: || : || :: || |::: |
59 TKYQISQPEVYVAAPGESLEVRCLLKDAAVISWTKDGVHLGPNNRTVLIGE-----
 Length 170;
 Length 281;
 35;
 37;
 8.4%; Score 63.5; DB 5;
20.6%; Pred. No. 0.98;
iive 11; Mismatches 37;
 DB 5;
 Query Match

8.5%; Score 64; DB 5;
Best Local Similarity 25.8%; Pred. No. 1.6;
Matches 23; Conservative 17; Mismatches 3:
 79 YNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYC 115
 -----YLQIKGATPRDSGLYAC 126
 103 SS----LTSEDSAVYYCA---RGGYDGWD 124
 143 ANAYVDLGTYGSITPYVGGGIGGSYVKWD 171
) ORGANISM: Agrobacterium tumefaciens US-09-739-449-11638
 Conservative
 Query Match
Best Local Similarity
Matches 20; Conserva
 TYPE: PRT
ORGANISM: Human
 ORGANISM: Human
 LENGTH: 170
 US-09-814-950-4
 US-09-814-950-4
 US-09-814-950-2
 SEQ ID NO 2
 TYPE: PRT
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 US-09-739-449-11638
US-09-739-449-11638
Sequence 11638, Application US/09739449
Sequence 11638, Application US/09739449
Sequence 11638
Sequence 11638
Sequence 11638
Sequence 11638
Sequences and Uses Thereof
TTPLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/739,449
SEQUENCE TILING DATE: 2000-12-19
SEQUENCE TILING DATE: 2000-02-23
NUMBER OF SEQUENCE 13351
SEQUENCE TILING DATE: 2000-02-33
SEQUENCE TILING DATE: 2000-02-33
SEQUENCE TILING DATE: 2000-02-33
SEQUENCE TILING DATE: 2000-02-33
SEQUENCE TILING DATE: 2010-02-33
SEQUENCE TILING DATE: 2010-02-33
SEQUENCE TILING DATE: 2010-02-33
 14;
 ë
 365 SDAASVGALAMVQLFQQSAK----ATGIDLGIKREPDDGY---WSNVWLKKPFCVSYW-N 416
 58 QRP-----GQGLEWIGEIDPSESNTNYNQKFKG---KATLTVDIS-SSTAYMQLS 103
 57 RVEIQRAG----EWGTICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGRIWLDNL 112
 Gaps
 12 STATSVH--SQVQLQQPGAELVKPGTSVKLSCK----GYGYTFTSYWM-----HWVK 57
 20 QVQLQQPGAELVKPGT-----SVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEI 70
 62;
 16;
 Length 517;
 Length 753;
 41; Indels
 Indels
 104 SLTSEDSA-----VYY-----CARGG----YDGWDYAIDYW 130
 33;
 Query Match
8.6%; Score 65; DB 5;
Best Local Similarity 24.7%; Pred. No. 2.5;
Matches 41; Conservative 22; Mismatches 4
 DB 1;
 Query Match

8.6%; Score 65; DB 1
Best Local Similarity 24.7%; Pred. No. 3.9;
Matches 21; Conservative 15; Mismatches
 SEGUENCE 1. APPLICATION PC/TUS0109226
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: PCT/US01/09226
CURRENT APPLICATION NUMBER: 60/192,158
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
 113 SCSGTEQSVTECASRGWGNSDCTHD 137
 71 DPS---ESNTNYNQKFKGKATLTVD 92
 ; ORGANISM: Homo sapiens
PCT-US01-09226-51
US-09-739-449-12328
 RESULT 12
PCT-US01-09226-51
 SEQ ID NO 51
LENGTH: 753
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Sequence 2, Application US/09814950
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEL, MING-HUL et al.
TITLE OF INVENTION: USCLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOOll14
CURRENT APPLICATION NUMBER: US/09/814,950
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SOFTHARE: FASTERE FASTERE FOR WINDOWS VETSION 4.0
 Length 172;
 Score 63.5;
Pred. No. 1;
 8.4%;
 Query Match
Best Local Similarity
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| ì                                                           |                                                                    |                                                         |                                             |                       |                                                                 |
|-------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------|---------------------------------------------|-----------------------|-----------------------------------------------------------------|
| ed po                                                       | TN 78                                                              | 109                                                     |                                             |                       |                                                                 |
| ,67                                                         | PSESN                                                              | 1 1 1 1                                                 |                                             |                       |                                                                 |
| THORTS                                                      | GLEWIGEID<br>                                                      | RTVLIGE-                                                |                                             |                       |                                                                 |
| . / 6                                                       | KORPGO                                                             | HLGPNN                                                  | 115                                         | 126                   |                                                                 |
| Mismarches                                                  | SYTETSYWMHWV!                                                      | DAAVISWTKDGVI                                           | FAYMQLSSLTSEDSAVYYC                         | YLQIKGATPRDSGLYAC 126 | :37:57                                                          |
| 11;                                                         | SCKGYO                                                             | RČLLKI                                                  | MQLSSI                                      | LQIKG                 | 1, 17                                                           |
| Matches 20; (Onservative 11; Mismarches 37; indexs 23; Gaps | 19 SQVQLQQFGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTN 78 | 59 TKYQISQI EVYVAAPGESLEVRCLLKDAAVISWTKDGVHLGPNNRTVLIGE | 79 YNQKFKGFATLTVDISSSTAYMQLSSLTSEDSAVYC 115 | X                     | Search completed: April 13, 2001, 17:37:57<br>Job time: 173 sec |
| 20;                                                         | SQVQLC                                                             | TKYOIS                                                  | YNQKFF                                      | 110                   | pletec<br>173 se                                                |
| atches                                                      | 19                                                                 | 59                                                      | 79                                          | 110                   | Search completed:<br>Job time: 173 sec                          |
| Σ                                                           | Qy                                                                 | qq                                                      | Qy                                          | QQ                    | Sea<br>Job                                                      |
|                                                             |                                                                    |                                                         |                                             |                       |                                                                 |

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

April 13, 2001, 15:36:11 ; Search time 28.17 Seconds (without alignments) 95.475 Million cell updates/sec Run on:

US-08-700-737-15 757 score: Title: Perfect :

1 MGWSCIILFLVSTATSVHSQ.......DGWDYAIDYWGQGTSVTVSS 140 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number, of hits satisfying chosen parameters:

185757 segs, 19210857 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
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/cgn2\_6/ptodata/2/laa/AB\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| •         |        | Description | :    | ,    | ,<br>, |      | ٠,    | ָ<br>ה<br>ה      | ,<br>, |                   | 18             | 0,00            | o c             |      | 9    | 0 0  | 0 0              |      | Ò,              | Sequence 4, Appli | àα              | ò c   | · (    | 9 6             | 7                | 7             | o,     | 7        | 'n             | -        |
|-----------|--------|-------------|------|------|--------|------|-------|------------------|--------|-------------------|----------------|-----------------|-----------------|------|------|------|------------------|------|-----------------|-------------------|-----------------|-------|--------|-----------------|------------------|---------------|--------|----------|----------------|----------|
| SUMMARIES |        | QI          |      |      |        |      |       | US-08-436-717-35 |        | US-08-553-497A-12 | US-08-482-882- | US-08-483-389-7 | US-08-487-113D- |      |      |      | US-08-714-017-78 |      | PCT-US93-11611- | US-08-253-877C-   | US-08-452-164A- | 0S-08 | 0.5-08 | US-08-428-257A- | 115-08-491-998-2 | - 000 101 000 | 4-00-4 | US-08-45 | US-08-491-988- | US-08-23 |
|           |        | Length DB   |      |      |        |      |       |                  | -      | ~                 | -              | N               | 7               | ~    | 7    | ~    |                  |      |                 | 139 1             |                 |       |        |                 |                  |               |        |          |                |          |
| æ         | Query  | Match       | 78.9 | 77.8 | 77.0   | 77.0 | 71.9  | 71.9             | 71.5   | 70.8              | 70.3           | 70.3            | 70.3            | 70.3 | 70.3 | 70.3 | 70.3             | 70.3 | 70.1            | 69.7              | 69.7            | 9.69  | 69.3   | 68.9            | 6.89             | 0             |        | 0.0      | 68.9           | 9.89     |
|           |        | Score       | 597  | 589  | 583    | 583  | 544.5 | 544.5            | 541    | 536               | 532            | 532             | 532             | 532  | 532  | 532  | 532              | 532  | 531             | 527.5             | 527.5           | 526.5 | 524    | 521.5           | 521.5            | 521 5         | 1.50   | 7        | 521.5          | 520.5    |
|           | Result | S.          | н    | ~    | m      | 4    | ហ     | φ.               | 7      | æ (               | on o           | 0 ;             | 11              | 12   | 13   | 14   | 15               | 16   | 17              | 18                | 19              | 20    | 21     | 22              | 23               | 24            | 2,5    | 3 6      | 0 0            | 7        |

| Sequence 9, Appli | ω,               |                  | Sequence 61 April | Section 63       | 5 -               | į                |                 | د<br>د ج         | Sequence 34, Appl | ,                 | , C               | 1                 | ,                  | 101               | 101,              | _                 | , A              |                 | • |  |
|-------------------|------------------|------------------|-------------------|------------------|-------------------|------------------|-----------------|------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|------------------|-----------------|---|--|
| PCT-US95-05262-9  | US-08-553-497A-8 | US-08-353-400-33 | US-08-881-037-61  | US-08-881-037-63 | PCT-US93-11611-11 | US-08-303-569B-7 | US-08-116-247-7 | US-08-513-968-34 | US-08-579-378A-12 | PCT-US93-11612-12 | US-07-634-278-101 | US-08-477-728-101 | 115-08-474-040-101 | 115-08-47-300-101 | TOT-007-104-00 CO | US-08-484-537-101 | US-08-881-037-60 | US-08-767-128-6 |   |  |
| 5                 | 7                | -                | ٣                 | ო                | 'n                | ~                | 7               | 4                | 4                 | S                 | 7                 | Н                 | -                  | •                 | 4 •               | 4                 | ო                | 4               |   |  |
| 122               | 119              | 445              | 119               | 119              | 136               | 468              | 468             | 151              | 140               | 140               | 152               | 152               | 152                | 152               | 1 6               | 7 C T             | 119              | 119             | , |  |
| 68.8              | 68.7             | 68.7             | 68.3              | 68.2             | 68.2              | 68.2             | 68.2            | 68.1             | 68.0              | 68.0              | 68.0              | 68.0              | 68.0               | 0 89              |                   | 080               | 67.8             | 67.8            |   |  |
| 520.5             | 520              | 520              | 517               | 516              | 516               | 516              | 516             | 515.5            | 515               | 515               | 515               | 515               | 515                | 515               | 2 1 2             | CTC               | 513              | 513             |   |  |
| 28                | 29               | 30               | 31                | 32               | 33                | 34               | 32              | 36               | 37                | 38                | 39                | 40                | 41                 | 42                |                   | 7                 | 44               | 45              |   |  |
|                   |                  |                  |                   |                  |                   |                  |                 |                  |                   |                   |                   |                   |                    |                   |                   |                   |                  |                 |   |  |

## ALIGNMENTS

SOFTWARE: Datentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 03-DEC-1993 FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS: Sequence 36, Application US/08353400 Patent No. 5665357 LENGTH: 464 amino acids TYPE: amino acid STRANDEDNESS: single ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-353-400-36 RESULT 1 US-08-353-400-36 ; Patent No.

Gaps ö ); Score 597; DB 1; Length 464; ); Pred. No. 3e-47; 11; Mismatches 17; Indels 78.9%; 80.0%; Query Match Best Local Similarity 80.0% Matches 112; Conservative

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121 DGWDYAIDYWGQGTSVTVSS 140 ô

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MONOCLONAL ANTIBODIES WHICH PROMOTE CENTRAL NERVOUS SYSTEM REMYELINATION
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTITE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINAT NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
 CLASSIFICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAV9
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-861-6240
 121 DGWDYAIDYWGQGTSVTVSS 140
 77.0%;
80.0%;
 STREET: Two Militia Drive
 TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
 Floppy disk
 143 amino acids
 Conservative
 SEQUENCE CHARACTERISTICS:
 Massachusetts
 COMPUTER READABLE FORM:
 protein
 Lexington
Massachusetts
 amino acid
 linear
 Query Match
Best Local Similarity
Matches 112; Conserv.
 Lexington
 TOPOLOGY: 111
MOLECULE TYPE:
 MEDIUM TYPE:
 ZIP: 02173
 RESULT 4
PCT-US95-05262-7
 COUNTRY:
 US-08-236-520-7
 STATE:
 Ω
 δλ
 qq
 δλ
 QQ
 ö
 61 GOGLEWI 3EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Gaps
 1 MGWSCIIJFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYMMHWVKQRP 60
 77.8%; Score 589; DB 1; Length 140;
80.7%; Pred. No. 4e-47;
Live 6; Mismatches 21; Indels
 Sequence 24, Application US/07946421
Patent No. 555864
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rettleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
 P.C.
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421 FILING DATE: 06 NOV-1992
 2200 Clarendon Boulevard, Suite 1400
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: WO PCT/EP92/00480
FILING DATH: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 911933892
FILING DATH: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
 Merck 1430
 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING (YSTEM: PC-DOS/MS-DOS
 Sequence 7, Application US/08236520 Patent No. 5591629 GENERAL INFORMATION:
 33,302
 REFERENCE/10CKET NUMBER: Me
TELECOMMUNIC, TION INFORMATION:
TELEPHONE: 703-243-6333
 121 DGWDYALDYWGQGTSVTVSS 140
 TELEX: 64.91
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
 121 DYDGRYFOYWGQGTTLTVSS 140
 Rodriguez, Moses
Miller, David J.
 NAME: Ham.et-King, Diana REGISTRATION NUMBER: 33,
 1.10 amino acids
 Query Match 77.8' Best Local Similarity 80.7' Matches 113; Conservative
 TELEPHONE: 703-243-6410
 NUMBER OF SECUENCES: 4
CORRESPONDENCE ADDRESS:
 STREET: 2200 ClarCITY: Arlington STATE: Virginia COUNTRY: U.S.A.
 amino acid
 ;
US-07-946-421-24
 ADDRESSEE:
 APPLICANT:
APPLICANT:
 US-08-236-520-7
 RESULT 2
US-07-946-421-24
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61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Sequence 7, Application PC/TUS9505262
Sequence 7, Application PC/TUS9505262
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMIELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Two Militia Drive
 Length 143;
 Indels
COMPUTER: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,520
CLASSIETT.
CLASSIETT.
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 Score 583; DB 1;
Pred. No. 1.4e-46;
 5; Mismatches
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61 GHGLEWIGELEPGTGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCASLDS 120
 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 24; Indels
 GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SALOHIK, Mary
APPLICANT: JONES, Steven
SALDANHA, JOSES, Steven
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREE: 3000 K Street, N.W., Suite 500
CITY: Washington
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINE: YETEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 71.9%; Score 544.5; DB 1
72.9%; Pred. No. 4.7e-43;
 Best Local Similarity 72.9%; pred. No. 4.7e-Matches 102; Conservative 13; Mismatches
 53466/126/AAOK
 CLASSIFICATION: 536
RICHARDA PAPLICATION DATA:
ARPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNET HATOID C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acids
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
 Sequence 35, Application US/08436717 Patent No. 5817790
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 SGY-YAMDYWGQGTSVTVSS 139
 MOLECULE TYPE: protein US-08-137-117D-35
 COUNTRY: USA
ZIP: 20007-5109
 TOPOLOGY:
 RESULT 6
US-08-436-717-35
 Query Match
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0
 61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 61 GGGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYYARRAP 120
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 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 77.0%; Score 583; DB 5; Length 143; 80.0%; Pred. No. 1.4e-46;
 23; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/137,117D
 GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
 CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricla
REGISTRATION NUMBER: 27,27
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFAX: 617-861-9540
 5; Mismatches
 FILING DATE: 20-DEC 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-320RA
APPLICATION NUMBER: JP 4-320RA
 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
APPLICATION NUMBER: PCT/US95/05262
 08-08-137-117D-35
; Sequence 35, Application US/08137117D
; Patent No. 5795965
 121 YYGSRNFDYWGQGTTLTVSS 140
 121 DGWDYAIDYWGQGTSVTVSS 140
 INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
 Best Local Similarity 80.0
Matches 112; Conservative
 ; TOPOLOGY: Ilnear
; MOLECULE TYPE: protein
PCT-US95-05262-7
 COUNTRY: USA
ZIP: 20007-5109
 STATE: D.C
 Query Match
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ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD. SUITE 1400 CITY: ARLINGTON
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17.NOV-1995
CLASSIFICATION: 530
 APPLICALLO...
FILING DATE: 17-NOV-LO...
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
---- NATE: 16-MAR-1995
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 12, Application US/08553497A Patent No. 5844093
 ABPELICANT: KETTLEBOROUGH, C. APPLICANT: BENDIG, MARY M.
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 YGGDWYFNVWGAGTTVTVSA 140
 TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 ANSELL, KEITH H.
 LENGTH: 140 amino acids TYPE: amino acid
 Matches 105; Conservative
 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-476-275-6
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, W
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Query Match
Best Local Similarity
 ZIP: 22201
 RESULT 8
US-08-553-497A-12
 APPLICANT:
 COUNTRY:
 STATE:
 qq
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 QΩ
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 // Witchell E.
// Asstetter, William H.
// Sastetter, William H.
// Sastetter, William H.
// Sastetter, Respective Application of Chimeric and
// SANTION: Rediolabeled Antibodies to Human B Lymphocyte Restricted
// SANTION: Differentiation Antigen for the Treatment of B-Cell
 ï
 61 GQGLEWIGEIDPSESNINYNQKFKGKATLIVDISSSTAYMQLSSLISEDSAVYYCARGGY 120
 61 GHGLEWI;EILPGTGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYXCASLDS 120
 1 MGWSGVF [FLLSVTAGVHSQVQLQQSGAELMKPGASVKISCKATGYTESSYWIVWIKQRP 60
 1 MGWSCII. FLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Length 139;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

* FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
 Query Match 71.9%; Score 544.5; DB 2; Best Local Simi.arity 72.9%; Pred. No. 4.7e-43; Matches 102; Conservative 13; Mismatches 24;
 NAME: WEGIER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/IOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERX: 202)672-5399
TELEX: 90.136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHAIRCTERISTICS:
LENGTH: 1:9 amino acids
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 619 Prince St. CITY: Alexandria
 MEDIUM TYP 2: Floppy disk
COMPUTER: IBM PC compatible
OPERATING 3YSTEM: PC-DOS/MS-DOS
 FILING DATH: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATH: 25-APR-1991
ATTORNEY/AGBHT INFORMATION:
NAME: WEGHER, HAROLD C.
APPLICATION NUMBER: JP 4-32084
FILING DATH: 19-FEB-1992
 Sequence 6, Application US/08476275
Patent No. 5776156
GENERAL INFORMITION:
 Anderson, Darrell R.
 121 DGWDYAIDYWGQGTSVTVSS 140
 121 SGY-YAM:)YWGQGTSVTVSS 139
 danna, Nabil
Jeonard, John E.
 : 139 amino acids
amino acid
 TITLE OF INVENTION: The TITLE OF INVENTION: Rad TITLE OF INVENTION: DIF TITLE OF INVENTION: Lymn NUMBER OF SEQUENCES: 11 CORRESPONDEN DE ADDRESS:
 ; MOLECULE TYPW: protein US-08-436-717-35
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 linear
 JSA
 TOPOLOGY:
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT:
 COUNTRY:
 US-08-476-275-6
 APPLICANT:
 STATE:
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 원
 ò
```

```
61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 71.5%; Score 541; DB 1; Length 140; 75.0%; Pred. No. 9.9e-43;
 10; Mismatches
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 05 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
 012712-155
 REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-836-6620
TELEFAX: 703-836-621
TELEFAX: 703-836-620
```

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Sequence 78, Application US/08483389
Patent No. 581517
GENERAL INFORMATION:
GENERAL THFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 23 South Wacker Drive/6300 Sears Tower
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
 APPLICATION NUMBER: US 08/009,266
FILING DATE: .22-JAN-1993
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 FILING DATE: 05-JUN-1
PRIOR APPLICATION DATA:
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-78
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Query Match
Best Local Similarity
Matches 103; Conserva
 US-08-483-389-78
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 ij
 80 NOKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCARGGYDGWDYALDYWGQGTSVTVS 139
 Gaps
 20 QVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRPGQGLEWIGEIDPSESNTNY 79
 Length 119;
 Sequence 78, Application US/08482882
Petent No. 5773218
CENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ZIP: 66606
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
 Score 536; DB 2;
Pred. No. 2.3e-42;
4; Mismatches 12;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY,AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
RECISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
 FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266 FILING DATE: 22-JAN-1993
 TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
 70.8%;
85.1%;
 Query Match
Best Local Similarity 85.1¹
Matches 103; Conservative
 / MOLECULE TYPE: protein US-08-553-497A-12
 PRIOR APPLICATION DATA
 TOPOLOGY: linear
 CITY: Chicago
STATE: Illinois
COUNTRY: USA
 US-08-482-882-78
 140 S 140
 119 S 119
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1 MGWSCIILFLVSTATSVHSOVOLQODGAELVKPGTSVKLSCKGYGYTFTSYMMHWVKORP 60
 70.3%; Score 532; DB 1; Length 138; larity 73.6%; Pred. No. 6.5e-42; Conservative 6; Mismatches 29; Indels
 APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA: WS 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773218and, Greta E.
REGISSRATION NUMBER: 35,302
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
 REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
 121 DGWDYAIDYWGQGTSVTVSS 140
 120 -GNSYGLDYWGQGTSVTVSS 138
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 APPLICATION NUMBER: US 08/009, 266
FILING DATE: 22-7AN-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894, 061
FILING DATE: 05-7UN-1992
RIING DATE: 05-7UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889, 724
FILING DATE: 26-MAY-1992
RIING DATE: 27-MAY-1992
ATTORNEY/AGENT INFORMATION:
AMAR: NO. 5837822ANG, Greta E.
REGISTRATION NUMBER: 35, 3074
REGISTRATION NUMBER: 35, 3074
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-7UN-1995
FILING DATE: 435
 US-08-473-503-78; Sequence 78, Application US/08473503; Patent No. 5869262
 REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
 120 -GNSYGLDYWGQGTSVTVSS 138
 121 DGWDYAIDYWGQGTSVTVSS 140
 Query Match 70.3%;
Best Local Similarity 73.6%;
Matches 103; Conservative (
 TELEPHONE: (312) 474-6300 (312) 474-6300 TELEFAX: 25-3856 INFORMATION FOR SEQ ID NO: 78
 : 138 amino acids
amino acid
 SEQUENCE CHARACTERISTICS
 , MOLECULE TYPE: protein US-08-487-113D-78
 FILING DATE: 07-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 linear
 90909
 LENGTH:
 δλ
 δλ
 61 GQGLEWIGYINPNTDYTEXNQRFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARWG- 119
 61 GOGLEWISEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 2; Gaps
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: (300 Sears Tower, 233 South Wacker Drive
 Indels
 Sequence 78, Application US/08487113D
Patent No. 58/37822
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INTENTION:
NUMBER OF SEQUENCES: 120
CORRESPONDERCE ADDRESS:
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPI,ICATION DATA:
APPLICATION NUMBER: US/08/487,113D
 29;
 Score 532; DB 2;
Pred. No. 6.5e-42;
 6; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATH:: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATH:: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATH:: 27-JAN-1992
ATTORNEY FAGENT THORMATION:
NAME: Suh Young J.
REGISTRATION NUMBER: P-41,337
REGISTRATION NUMBER: 27866/32760
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN:: 312) 474-6300
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DAME: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
 STATE: Illinois
COUNTRY: United States of America
ZIP: 606(.6-6402
 COMPUTER RELDABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 121 DGWDYAIDYWGQGTSVTVSS 140
 120 -GNSYGLDYWGQGTSVTVSS 138
 TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 78:
 70.3%;
| larity 73.6%;
| Sonservative
 : 138 amino acids
amino acid
 SEQUENCE CHARACTERISTICS LENGTH: 138 amino acic
 protein
 Query Match
Best Local Similarity
Matches 103; Jonserva
 linear
 STREET: (300 S
CITY: Chicago
 MOLECULE TYP3:
 FILING DATE:
 US-08-487-113D-7E
 TOPOLOGY:
 US-08-483-389-78
 RESULT 11
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61 GOGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 61 GGGLEWIGYINPNTDYTEYNORFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARWG- 119
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 Gaps
 5;
 GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazenx, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: G300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
 Length 138;
Score 532; DB 2; Length 13
Pred. No. 6.5e-42;
6; Mismatches 29; Indels
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CLASSIFICATION:
 LENGTH:
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 Gaps
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 ;
 Sequence 78, Application US/08483932
Patent No. 5880268
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
CTTY: Chicago
STATE: Illinois
COUNTRY: USA
 Score 532; DB 2; Length 138;
Pred. No. 6.5e-42;
6; Mismatches 29; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
 FILING DATE: U3-AUG-1233

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/89,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT IMPORMATION:
NAME: NO. 5869262and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3178
TELECHONE: (312) 474-6300
TELECHONE: (312) 474-6300
TELEFAX: (312) 474-6448

INPORMATION FOR SEQ ID NO: 78:
 JAMBER: US 08/102,852
05-AUG-1993
 APPLICATION NUMBER: US/08/483,932
 120 -GNSYGLDYWGQGTSVTVSS 138
 121 DGWDYAIDYWGQGTSVTVSS 140
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Best Local Similarity 73.6%;
Matches 103; Conservative
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08
 LENGTH: 138 amino acids TYPE: amino acid
 SEQUENCE CHARACTERISTICS
 ; MOLECULE TYPE: protein US-08-473-503-78
 linear
 90909
 ropology:
 US-08-483-932-78
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1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 RESULT 14
US-08-720-420A-78
Sequence 78, Application US/08720420A
Sequence 78, Application US/08720420A
Sequence 78, Application US/08720420A
Sequence 78, Application US/08720420A
Sequence 78, Application:
APPLICANT: Vazeux, Nosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall: O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STREET: 6100 Sears Tower, 233 South Wacker Drive COUNTRY: United States of America
STATE: Illinois
COUNTRY: United States of America
STREET: 6606-6402
COUNTRY: United States of America
STREET: 6006-6402
COUNTRY: UNITED STATES: STATES: STATES: ILLINOIS
COUNTRY: UNITED STATES: STAT
 Length 138;
 Score 532; DB 2; Length 13:
Pred. No. 6.5e-42;
6; Mismatches 29; Indels
 Gerstein, Murray & Borun
South Wacker Drive
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: 08 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UNN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5880266and, Greta E.
REGISTRATION NUMBER: 33178
TELECOMMUNICATION INFORMATION:
MAME: NO. 5880266and, Greta E.
REGISTRATION NUMBER: 33178
TELECOMMUNICATION INFORMATION:
 121 DGWDYAIDYWGQGTSVTVSS 140
 -GNSYGLDYWGQGTSVTVSS 138
 TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELES: 25-3856
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
 70.3%;
73.6%;
 : 138 amino acids
amino acid
 Query Match
Best Local Similarity 73.6
Matches 103; Conservative
 , MOLECULE TYPE: protein US-08-483-932-78
 linear
 TOPOLOGY:
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
 , MOLECULE TYPE:
US-08-714-017-78
 FOPOLOGY:
 δλ
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 1;
 61 GQGLEWI3EIDPSESNTNYNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 1 MGWSCIILFLVSTATSVHSQVQLQQPGAELVKPGTSVKLSCKGYGYTFTSYWMHWVKQRP 60
 2;
 Length 138;
 Sequence 78, Application US/08714017
Patent No. 604C176
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: VAZEUX, ROSEMBY
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: MAISHALL, O'Toole, Gerstein, Murray & Borun
STREET: (300 Sears Tower, 233 S. Wacker Drive
 Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPL:CATION DATA:
APPLICATION NUMBER: US/08/720,420A
 Score 532; DB 2;
Pred. No. 6.5e-42;
6; Mismatches 29
 FILING DATH: 26-JAW PER PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061
FILING DATH: 05-JUN-1992
PRIOR APPLICATION DATA: 36-JUN-1992
PRIOR APPLICATION DATA: 26-MAY-1992
FILING DATH: 26-MAY-1992
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 37-JAN-1992
ATTORNEY, AGG TH THORMATION:
NAME: WILLIAMS, JOSEPH A., JF. REGISTRATION NUMBER: 38,659
REFERENCE/ NOKET NUMBER: 33.282
TELECHONE: (312) 474-6300
TELECHONE: (312) 474-6300
TELECHONE: (312) 474-6300
TELECHONE: ASSOCIATION OF SEQUENCE CARRACTERS: 1866
INFORMATION FOR SEQ ID NO: 78: SEQUENCE CHARACTERS: 188 and 100 acids

LENGTH: 188 and 100 acids
 FILING DATH:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
FILING DATH: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATH: 05-AUG-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATH: US 08/102,852
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATH: 22-JAN-1993
 121 DGWDYAIDYWGQGTSVTVSS 140
 120 -GNSYGLDYWGQGTSVTVSS 138
 70.3%;
73.6%;
 Query Match 70.33
Best Local Similarity 73.65
Matches 103; Conservative
 protein
 STREET: (300 (CITY:, Chicago
 US-08-720-420A-78
 RESULT 15
US-08-714-017-78
 TOPOLOGY:
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 qq
 δ
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61 GOGLEWIGYINPNTDYTEYNORFQDKATLTADKSSSTAXMQLSSLTSEDSAVYXCARWG- 119
 61 GOGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Length 138;
 29; Indels
SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/71
 Score 532; DB 3;
Pred. No. 6.5e-42;
6; Mismatches 29;
 PAPLILEATION NUMBER: CLASSIFICATION:
PRICR APPLICATION DATE:
APPLICATION NUMBER: 08/286,754
FILING DATE: 08/286,754
FILING DATE: 08/20193
PRICR APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AGG-1993
PRICR APPLICATION DATA: US 08/009,266
FILING DATE: 22-JAN-1993
PRICR APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-JAN-1993
PRICR APPLICATION DATA: US 07/894,061
FILING DATE: 26-MAY-1992
PRICR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 3178
TELECOMMUNICATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 3178
TELECOMMUNICATION NUMBER: 32178
 Search completed: April 13, 2001, 15:36:11 Job time: 129 sec
 121 DGWDYAIDYWGQGTSVTVSS 140
 Query Match 70.3%;
Best Local Similarity 73.6%;
Matches 103; Conservative
 SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
 protein
 amino acid
 inear.
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